

FORM PTO-1390  
(REV 10-95)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1768

U.S. APPLICATION NO (If known, see 37 CFR §1.5)

**09/646778**

INTERNATIONAL APPLICATION NO

INTERNATIONAL FILING DATE

PRIORITY DATE CLAIMED

PCT/DE99/01087

7 APRIL 1999

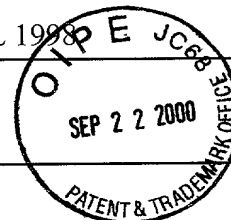
9 APRIL 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

APPLICANT(S) FOR DO/EO/US

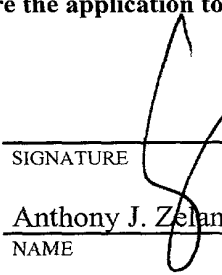
SPECHT, Thomas, et al.

**Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:**

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19<sup>th</sup> month from the earliest claimed priority date
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
  - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☒ has been transmitted by the International Bureau.
  - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
  - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. ☐ have been transmitted by the International Bureau.
  - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
  - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

**Items 11. to 16. below concern document(s) or information included:**

11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
  - ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☐ Other items or information:

U.S. APPLICATION NO. (if known, see 37 CFR §1.5) <b>09/646778</b>		INTERNATIONAL APPLICATION NO. PCT/DE99/01087		ATTORNEY'S DOCKET NUMBER SCH 1768	
17. <input checked="" type="checkbox"/> The following fees are submitted: <b>BASIC NATIONAL FEE ( 37 CFR §1.492 (a) (1) - (5)):</b> Search Report has been prepared by the EPO or JPO..... \$840.00 International preliminary examination fee paid to USPTO (37 CFR §1.482)..... \$670.00 No international preliminary examination fee paid to USPTO (37 CFR §1.482) but international search fee paid to USPTO (37 CFR §1.445(a)(2))..... \$760.00 Neither international preliminary examination fee (37 CFR §1.482) nor international search fee (37 CFR §1.445(a)(2)) paid to USPTO..... \$970.00 International preliminary examination fee paid to USPTO (37 CFR §1.482) and all claims satisfied provisions of PCT Article 33(2)-(4)..... \$96.00  <div style="text-align: right;"><b>ENTER APPROPRIATE BASIC FEE AMOUNT =</b> \$840.00</div>				<b>CALCULATIONS</b> PTO USE ONLY	
Surcharge of \$130.00 for furnishing the oath or declaration later than months from the earliest claimed priority date (37 C.F.R. §1.492(e)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	41 - 20 =	21	x \$ 18.00	\$378.00	
Independent claims	7 - 3 =	4	x \$ 78.00	\$312.00	
MULTIPLE DEPENDENT CLAIM(S) (if applicable)			+ \$ 260.00		
<b>TOTAL OF ABOVE CALCULATIONS =</b>				\$1,530.00	
Reduction of 1/2 for filing by small entity, if applicable. A Verified Small Entity Statement must also be filed (Note 37 C.F.R. §§1.9, 1.27, 1.28).					
<b>SUBTOTAL =</b>				\$1,530.00	
Processing fee of \$130.00 for furnishing the English translation later than months from the earliest claimed priority date (37 C.F.R. §1.492(f)). <input type="checkbox"/> 20 <input type="checkbox"/> 30					
<b>TOTAL NATIONAL FEE =</b>				\$1,530.00	
Fee for recording the enclosed assignment (37 C.F.R. §1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 C.F.R. §§3.28, 3.31). \$40.00 per property.					
<b>TOTAL FEES ENCLOSED =</b>				\$1,530.00	
				Amount to be refunded:	
				charged:	
a. <input checked="" type="checkbox"/> A check in the amount of <u>\$1,530.00</u> to cover the above fees is enclosed. b. <input type="checkbox"/> Please charge my Deposit Account No. <u>13-3402</u> in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed. c. <input checked="" type="checkbox"/> The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. <u>13-3402</u> . A duplicate copy of this sheet is enclosed.					
<b>NOTE: Where an appropriate time limit under 37 C.F.R. §§1.494 or 1.495 has not been met, a petition to revive (37 C.F.R. §1.137(a) or (b)) must be filed and granted to restore the application to pending status.</b>					
SEND ALL CORRESPONDENCE TO: MILLEN, WHITE, ZELANO & BRANIGAN, P.C. Arlington Courthouse Plaza I 2200 Clarendon Boulevard, Suite 1400 Arlington, Virginia 22201 (703) 243-6333					
Filed: 22 SEPTEMBER 2000 AJZ:jmm			SIGNATURE  NAME Anthony J. Zelano		
			27,969 REGISTRATION NUMBER		

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE

International Application No. : PCT/DE99/01087  
International Filing Date : 7 APRIL 1999  
Priority Date(s) Claimed : 9 APRIL 1998  
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE

**PRELIMINARY AMENDMENT**

Commissioner for Patents  
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

**IN THE CLAIMS:**

- Claim 5, line 3, after "258-273" insert --of Claim 3--;
- Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 7, line 1, delete "claims 1 to 4" and insert --Claim 3--;
- Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 10, line 1, delete "claims 1 to 7" and insert --Claim 3--;
- Claim 11, lines 1 and 2, delete "one of claims 1 to 10" and insert --Claim 3--;
- Claim 12, line 2, delete "one of claims 1 to 10" and insert --Claim 3--;
- Claim 14, lines 1 and 2, delete "one of claims 12 and 13" and insert --Claim 12--;
- Claim 15, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;
- Claim 17, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;
- Claim 19, line 1, delete "one of claims 17 or 18" and insert --Claim 17--;
- Claim 20, line 2, delete "claims 17 to 19" and insert --Claim 17--;

Claim 31, line 2, after "258-273" insert --of Claim 3--;  
Claim 32, line 2, after "258-273" insert --of Claim 3--;  
Claim 33, line 2, after "agents" insert --of Claim 35--;  
Claim 34, line 2, after "agent" insert --of Claim 35--;  
Claim 36, line 1, delete "claims 1 to 10" and insert --Claim 3--;  
Claim 37, line 1, delete "claims 1 to 10" and insert --Claim 3;  
Claim 38, line 4, after "258-273" insert --of Claim 3--;  
Claim 41, line 1, delete "claims 1 to 7" and insert --Claim 3--.

8. (Amended) A nucleic acid sequence comprising a portion of the nucleic acid sequences named in [claims 1 to 6] claim 3, in such a sufficient amount that they hybridize with the sequences according to [claims 1 to 7] claim 3 or a sequence having 90% homology thereto.

#### REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Respectfully submitted,

  
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AJZ:jmm



### Human Nucleic Acid Sequences from Ovarian Tumor Tissue

The invention relates to human nucleic acid sequences from ovarian tumor tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main cancer causes of death in women is ovarian cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer ( $> 2000$  nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which play a role as candidate genes in ovarian cancer, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273,
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID Nos. 1-123 and 258-273, which are expressed elevated in ovarian tumor tissue.

The invention also relates to nucleic acid sequences Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108, and 112, which are expressed elevated in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia), 2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as *E. coli* or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 124-257 and 274-307.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 124-257 and 274-307 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The invention also relates to phage-display phages, which are directed against a polypeptide or a fragment and which are coded by the nucleic acids of sequences Seq. ID Nos. 1-123 and 258-273 according to the invention.

The polypeptides of sequences Seq. ID Nos. 124-257 and 274-305 according to the invention can also be used as tools for finding active ingredients against ovarian cancer, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides, which can be used as tools for finding active ingredients against ovarian cancer.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID Nos. 124-257 and 274-305 as pharmaceutical agents in the gene therapy for treatment of ovarian cancer or for the production of a pharmaceutical agent for treatment of ovarian cancer.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-305.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-123 and 258-273 for use as vehicles for gene transfer.



## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes).

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus).

Singleton = A contig that contains only one sequence.

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins.

N = selectively the nucleotide A, T, G or C.

X = selectively one of the 20 naturally occurring amino acids.

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

maximum percent mismatch = maximum deviation in %

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for tumor-related candidate genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

Figures 2b1-2b4 illustrate the lengthening of the ovarian tumor tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

**Example 2****Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 68 was found which occurs 6.08 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 68

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0141	0.0244	0.5758	1.7366
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0126	0.0082	1.5299	0.6536
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0847	0.1300	7.6946
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0233	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0143	0.4355	2.2964
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0153	0.0043	3.5827	0.2791
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0147			
Cervix	0.0426			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0178	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0259
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0121	Nerves	0.0479
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

**2.1.2**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 86 was found which occurs 7.82 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:



Electronic Northern for SEQ. ID NO.: 86

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0128	0.9153	1.0926
Breast	0.0090	0.0169	0.5293	1.8893
Small intestine	0.0092	0.0331	0.2781	3.5964
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0204	0.0426	0.4795	2.0856
Gastrointestinal	0.0211	0.0185	1.1390	0.8780
Brain	0.0274	0.0195	1.4020	0.7133
Hematopoietic	0.0107	0.1136	0.0941	10.6267
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0307	0.0137	2.2358	0.4473
Testicles	0.0115	0.0819	0.1406	7.1142
Lung	0.0104	0.0286	0.3629	2.7557
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0342	0.4758	2.1016
Pancreas	0.0132	0.0110	1.1966	0.8357
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0270	0.5277	0.0512	19.5264
Uterus-myometrium	0.0229	0.0408	0.5611	1.7821
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0000			
Sensory organs	0.0353			
White blood cells	0.0095			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0696	Ovary_n	0.0000
Brain	0.0167	Ovary_t	0.0000
Hematopoietic	0.0626	Endocrine tissue	0.0245
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0285	Skin-muscle	0.0097
Suprarenal gland	0.0072	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0062	Nerves	0.0000
Prostate	0.0303	Prostate	0.0155
Sensory organs	0.0997	Sensory Organs	0.0000
	0.0126	Uterus_n	

**2.1.3**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 114 was found which occurs 6.94 x more heavily in normal ovarian tissue than in tumor tissue.

The result is as follows:

Electronic Northern for SEQ. ID NO.: 114

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0136	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0064	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0445			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.1418
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0047
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0062	Testicles	0.0000
Kidney		Lung	0.0154
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0137
		Uterus_n	0.0000

In an analogous procedure, the following Northernblots were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0179	0.0075	2.3818	0.4198
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0059	0.0103	0.5760	1.7362
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0129	0.7353	1.3600
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0052	0.0164	0.3175	3.1494
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0061			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0125	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels		Hematopoietic	0.0057
Lung	0.0142	Skin-muscle	0.0032
Suprarenal gland	0.0145	Testicles	0.0154
Kidney	0.0254	Lung	0.0164
Placenta	0.0000	Nerves	0.0141
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

## Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS  
% frequency

Development  
Gastrointestinal  
Brain  
Hematopoietic  
Skin  
Hepatic  
Heart-blood vessels  
Lung  
Suprarenal gland  
Kidney  
Placenta  
Prostate  
Sensory organs

0.0139  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000  
0.0000

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Breast  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles  
Lung  
Nerves  
Prostate  
Sensory Organs  
Uterus\_n

0.0000  
0.0000  
0.0000  
0.0000  
0.0035  
0.0000  
0.0171  
0.0194  
0.0000  
0.0082  
0.0020  
0.0137  
0.0000  
0.0000

Electronic Northern for SEQ. ID NO.: 3

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0026	4.5763	0.2185
Breast	0.0064	0.0019	3.4026	0.2939
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0085	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0178			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0065
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 4

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0026	0.0000 undef	
Small intestine	0.0051	0.0000	undef 0.0000	
Ovary	0.0000	0.0000	undef undef	
Endocrine tissue	0.0000	0.0572	0.0000 undef	
Gastrointestinal	0.0034	0.0075	0.4528 2.2083	
Brain	0.0019	0.0093	0.2071 4.8289	
Hematopoietic	0.0022	0.0021	1.0799 0.9260	
Skin	0.0013	0.0379	0.0353 28.3379	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0065	0.0000 undef	
Testicles	0.0053	0.0000	undef 0.0000	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0104	0.0041	2.5402 0.3937	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0017	0.0000	undef 0.0000	
Pancreas	0.0027	0.0000	undef 0.0000	
Penis	0.0083	0.0000	undef 0.0000	
Prostate	0.0030	0.0000	undef 0.0000	
Uterus-endometrium	0.0022	0.0000	undef 0.0000	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000	0.0000	undef undef	
Breast hyperplasia	0.0128	0.0000	undef 0.0000	
Prostate hyperplasia	0.0000	0.0000	undef 0.0000	
Seminal vesicle	0.0089	0.0000	undef 0.0000	
Sensory organs	0.0000	0.0035	undef 0.0000	
White blood cells	0.0035	0.0106		
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0142	Skin-muscle	0.0065
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0060
Placenta	0.0062	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0208
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0075	1.8715	0.5343
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0390	0.3070	3.2573
Endocrine tissue	0.0290	0.0376	0.7698	1.2990
Gastrointestinal	0.0211	0.0324	0.6508	1.5365
Brain	0.0126	0.0144	0.8742	1.1439
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0218	0.0204	1.0669	0.9373
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0137	0.0000	undef	0.0000
Kidney	0.0190	0.0205	0.9252	1.0808
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0408	0.3741	2.6732
Uterus-general	0.0306	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0217			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0476
Gastrointestinal	0.0557	Ovary_n	0.3190
Brain	0.0167	Ovary_t	0.0101
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0151
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0213	Skin-muscle	0.0000
Suprarenal gland	0.0181	Testicles	0.0309
Kidney	0.0254	Lung	0.0082
Placenta	0.0185	Nerves	0.0010
Prostate	0.0121	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0310
	0.0251	Uterus_n	0.0458

Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000 undef	
Breast	0.0026	0.0113	0.2268 4.4083	
Small intestine	0.0031	0.0331	0.0927 10.7893	
Ovary	0.0000	0.0182	0.0000 undef	
Endocrine tissue	0.0051	0.0050	1.0189 0.9815	
Gastrointestinal	0.0057	0.0139	0.4142 2.4145	
Brain	0.0030	0.0010	2.8798 0.3472	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0065	0.0000 undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0062	0.0123	0.5080 1.9684	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0163	0.0205	0.7930 1.2610	
Kidney	0.0017	0.0055	0.2991 3.3428	
Pancreas	0.0030	0.0000	undef 0.0000	
Penis	0.0000	0.0021	0.0000 undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0064	0.0000	undef undef	
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0052
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0120
Prostate	Prostate 0.0205
Sensory organs	Sensory Organs 0.0077
	Uterus_n 0.0042

Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0064	0.0038	1.7013 0.5878	
Small intestine	0.0031	0.0000	undef 0.0000	
Ovary	0.0000	0.0156	0.0000 undef	
Endocrine tissue	0.0068	0.0125	0.5434 1.8403	
Gastrointestinal	0.0000	0.0046	0.0000 undef	
Brain	0.0037	0.0000	undef 0.0000	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0065	0.0000 undef	
Heart	0.0042	0.0137	0.3084 3.2426	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0031	0.0000	undef 0.0000	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0000	0.0060	0.0000 undef	
Muscle-skeleton	0.0054	0.0068	0.7930 1.2610	
Kidney	0.0050	0.0000	undef 0.0000	
Pancreas	0.0120	0.0000	undef 0.0000	
Penis	0.0022	0.0000	undef 0.0000	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0068	0.0000 undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0089			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0026			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0333

Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0038	0.0019	2.0416 0.4898	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0000	0.0208	0.0000 undef	
Endocrine tissue	0.0034	0.0201	0.1698 5.8889	
Gastrointestinal	0.0057	0.0000	undef 0.0000	
Brain	0.0081	0.0072	1.1314 0.8839	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0037	0.0000	undef 0.0000	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0021	0.0000	undef 0.0000	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0010	0.0020	0.5080 1.9684	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0051	0.0000	undef 0.0000	
Kidney	0.0054	0.0000	undef 0.0000	
Pancreas	0.0017	0.0000	undef 0.0000	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0065	0.0043	1.5354 0.6513	
Uterus-endometrium	0.0068	0.1583	0.0427 23.4317	
Uterus-myometrium	0.0152	0.0000	undef 0.0000	
Uterus-general	0.0051	0.0000	undef 0.0000	
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0036	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0100
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0009			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0102	0.0038	2.7221	0.3674
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0170	0.0201	0.8491	1.1778
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0126	0.0072	1.7485	0.5719
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0093	0.0061	1.5241	0.6561
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0137	0.0180	0.7615	1.3133
Kidney	0.0054	0.0479	0.1133	8.8268
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0150	0.0000	undef	0.0000
Prostate	0.0087	0.0021	4.0945	0.2442
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal		Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0083	Endocrine tissue	0.0000
Skin	0.0063	Fetal	0.0000
Hepatic	0.0118	Gastrointestinal	0.0057
Heart-blood vessels	0.0000	Hematopoietic	0.0259
Lung	0.0107	Skin-muscle	0.0154
Suprarenal gland	0.0072	Testicles	0.0082
Kidney	0.0000	Lung	0.0040
Placenta	0.0247	Nerves	0.0205
Prostate	0.0182	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0042
	0.0000	Uterus_n	

Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0026	0.0019	1.3611	0.7347
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0020	0.5080	1.9684
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0055	0.0000	undef
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0021	2.0473	0.4885
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0051	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0015	0.0010	1.4399	0.6945
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0020	1.0161	0.9842
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0086	0.0120	0.7139	1.4008
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0087	0.0064	1.3648	0.7327
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0035			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0061	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0179	0.6538	1.5296
Breast	0.0307	0.0226	1.3611	0.7347
Small intestine	0.0215	0.0000	undef	0.0000
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0034	0.0050	0.6792	1.4722
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0074	0.0133	0.5538	1.8057
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0148	0.0137	1.0794	0.9265
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0353	0.0164	2.1591	0.4631
Stomach-esophagus	0.0387	0.0077	5.0421	0.1983
Muscle-skeleton	0.0154	0.0120	1.2850	0.7782
Kidney	0.0163	0.0274	0.5948	1.6813
Pancreas	0.0198	0.0166	1.1966	0.8357
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0064	3.0709	0.3256
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0178			
Sensory organs	0.0353			
White blood cells	0.0182			
Cervix	0.0426			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0051
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0249	Hematopoietic	0.0114
Lung	0.0181	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0110
Prostate	0.0499	Prostate	0.0274
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0458

Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0000	0.0125	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0044	0.0021	2.1599	0.4630
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0104	0.0041	2.5402	0.3937
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0021	1.0236	0.9769
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0096			
Uterus-general	0.0000			
Breast hyperplasia	0.0083			
Prostate hyperplasia	0.0060			
Seminal vesicle	0.0022			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0017			
	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0259
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0062	Lung	0.0100
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0251	Sensory Organs	0.0333
		Uterus n	

## Electronic Northern for SEQ. ID NO.: 19

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0050	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0020	0.0000	undef
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0065
Lung	0.0000	Skin-muscle	0.0077
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0073	0.0020	3.5562	0.2812
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0050	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0044	0.0021	2.0473	0.4885
Penis	0.0068	0.0000	undef	0.0000
Prostate	0.0076	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0032			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0061			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 21

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0015	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0155
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 22

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0165	0.0000	undef
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0068	0.0000	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0051	0.0019	2.7221	0.3674
Small intestine	0.0031	0.0331	0.0927	10.7893
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0096	0.0093	1.0354	0.9658
Brain	0.0059	0.0021	2.8798	0.3472
Hematopoietic	0.0000	0.0379	0.0000	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0042	0.0061	0.6774	1.4763
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0017			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 24

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0077	2.5424	0.3933
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0153	0.0226	0.6792	1.4722
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0081	0.0092	0.8800	1.1364
Hematopoietic	0.0067	0.0379	0.1764	5.6676
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0102	0.8129	1.2302
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0103	0.0180	0.5711	1.7510
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0329	0.0000	undef	0.0000
Prostate	0.0153	0.0064	2.3885	0.4187
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0305	0.0136	2.2445	0.4455
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0069			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0136
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0157	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0171
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0246
Kidney	0.0121	Lung	0.0060
Placenta	0.0249	Nerves	0.0205
Prostate	0.0000	Prostate	0.0387
Sensory organs		Sensory Organs	0.0250
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0263	0.5347	1.8702
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0090	0.0312	0.2878	3.4745
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0222	0.0113	1.9635	0.5093
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0129	0.3676	2.7200
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0135	0.0123	1.1007	0.9085
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0188	0.0300	0.6282	1.5918
Kidney	0.0163	0.0205	0.7930	1.2610
Pancreas	0.0083	0.0221	0.3739	2.6743
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0102	0.0954	0.1067	9.3678
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0058
Hepatic	0.0260	Gastrointestinal	0.0488
Heart-blood vessels	0.0107	Hematopoietic	0.0114
Lung	0.0072	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0124	Lung	0.0164
Placenta	0.0000	Nerves	0.0060
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 26

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0204	1.1441	0.8741
Breast	0.0192	0.0470	0.4083	2.4491
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0090	0.0546	0.1645	6.0803
Endocrine tissue	0.0204	0.0075	2.7170	0.3681
Gastrointestinal	0.0268	0.0416	0.6443	1.5522
Brain	0.0037	0.0154	0.2400	4.1669
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0476	0.0259	1.8382	0.5440
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0166	0.0184	0.9032	1.1072
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0069	0.0300	0.2284	4.3775
Kidney	0.0543	0.0411	1.3217	0.7566
Pancreas	0.0363	0.0110	3.2906	0.3039
Penis	0.0060	0.0267	0.2246	4.4517
Prostate	0.0218	0.0128	1.7060	0.5862
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0535			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0078			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0204
Gastrointestinal	0.0083	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0040
Placenta	0.0121	Nerves	0.0137
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 27

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0074	0.0051	1.4399	0.6945
Hematopoietic	0.0027	0.0379	0.0706	14.1689
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Hepatic	0.0032	0.0000	undef	0.0000
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0054	0.0068	0.7930	1.2610
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0128	0.1706	5.8615
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0000	Nerves	0.0030
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 28

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0090	0.0038	2.3818	0.4198
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0100	1.1887	0.8413
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0015	0.0031	0.4800	2.0835
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0041	0.2540	3.9367
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0109	0.0043	2.5591	0.3908
Uterus-endometrium	0.0068	0.0528	0.1280	7.8106
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0217	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0030
Placenta	0.0121	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0021	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0051	0.0000	undef	0.0000
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0009			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0032
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0026	3.0509	0.3278
Breast	0.0038	0.0113	0.3403	2.9389
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0030	0.0702	0.0426	23.4526
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0556	0.0278	2.0018	0.4995
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0323	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0062	0.0082	0.7621	1.3122
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0110	0.0000	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0255	0.2559	3.9077
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0192			
Uterus-general	0.0357			
Breast hyperplasia	0.0890			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0213			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0167	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0000	0.0019	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0000	0.0010	0.0000	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0123	0.1693	5.9051
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 32

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0075	0.5104	1.9593
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0153	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0118			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 33

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0741	0.8942	1.1183
Breast	0.0640	0.0846	0.7561	1.3225
Small intestine	0.1104	0.0165	6.6733	0.1499
Ovary	0.0958	0.1951	0.4912	2.0358
Endocrine tissue	0.0511	0.0426	1.1987	0.8343
Gastrointestinal	0.1188	0.1527	0.7781	1.2851
Brain	0.0584	0.0863	0.6771	1.4769
Hematopoietic	0.1016	0.1136	0.8940	1.1186
Skin	0.0698	0.0000	undef	0.0000
Hepatic	0.0048	0.0776	0.0613	16.3199
Heart	0.1304	0.0000	undef	0.0000
Testicles	0.0230	0.0819	0.2811	3.5571
Lung	0.1620	0.1227	1.3209	0.7571
Stomach-esophagus	0.0580	0.1073	0.5402	1.8511
Muscle-skeleton	0.1045	0.0480	2.1773	0.4593
Kidney	0.0516	0.0959	0.5381	1.8583
Pancreas	0.0529	0.1491	0.3545	2.8205
Penis	0.0749	0.0800	0.9360	1.0684
Prostate	0.0632	0.0426	1.4843	0.6737
Uterus-endometrium	0.0676	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.2309	0.4621	2.1640
Uterus-general	0.1528	0.0000	undef	0.0000
Breast hyperplasia	0.0480			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0534			
Sensory organs	0.0235			
White blood cells	0.1309			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0333	Ovary_t	0.1595
Hematopoietic	0.0626	Endocrine tissue	0.0152
Skin	0.0590	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0052
Heart-blood vessels	0.0260	Hematopoietic	0.0244
Lung	0.0391	Skin-muscle	0.0000
Suprarenal gland	0.0650	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0432	Nerves	0.0573
Prostate	0.0424	Prostate	0.0181
Sensory organs	0.0249	Sensory Organs	0.0342
	0.0126	Uterus_n	0.0000
			0.0333

Electronic Northern for SEQ. ID NO.: 34

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0038	0.0000	undef	0.0000
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0598	0.0501	19.9782
Endocrine tissue	0.0068	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0042	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0299	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0106			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 35

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000 undef	
Breast	0.0000	0.0038	0.0000 undef	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0030	0.0234	0.1279 7.8175	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0192	0.0185	1.0354 0.9658	
Brain	0.0015	0.0062	0.2400 4.1669	
Hematopoietic	0.0013	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0052	0.0061	0.8467 1.1810	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0000	0.0060	0.0000 undef	
Muscle-skeleton	0.0027	0.0000	undef 0.0000	
Kidney	0.0000	0.0110	0.0000 undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000			
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0051
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 36

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0000	undef	0.0000
Small intestine	0.0026	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0025	0.0000	undef
Brain	0.0000	0.0139	0.0000	undef
Hematopoietic	0.0022	0.0000	undef	0.0000
Skin	0.0027	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0137	0.0000	undef
Lung	0.0000	0.0234	0.0000	undef
Stomach-esophagus	0.0021	0.0020	1.0161	0.9842
Muscle-skeleton	0.0000	0.0153	0.0000	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 38

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0000	0.0000	undef undef	
Small intestine	0.0000	0.0000	undef undef	
Ovary	0.0000	0.0234	0.0000 undef	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0000	0.0000	undef undef	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0000	0.0000	undef undef	
Testicles	0.0000	0.0000	undef undef	
Lung	0.3189	0.0153	20.7988	0.0481
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0000	0.0000	undef undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0000
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0000
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0000
Placenta	Nerves 0.0000
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0083
	Uterus_n

Electronic Northern for SEQ. ID NO.: 39

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0286	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0030	0.0072	0.4114	2.4307
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0058	0.0117	0.4920	2.0326
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0097	0.0077	1.2605	0.7933
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0054	0.0137	0.3965	2.5219
Kidney	0.0033	0.0000	undef	0.0000
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0022	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0059			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0043			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0062	Nerves	0.0020
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0291

Electronic Northern for SEQ. ID NO.: 40

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0077	0.5085	1.9666
Small intestine	0.0051	0.0056	0.9074	1.1021
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0030	0.0208	0.1439	6.9489
Gastrointestinal	0.0102	0.0025	4.0755	0.2454
Brain	0.0115	0.0093	1.2425	0.8048
Hematopoietic	0.0044	0.0062	0.7200	1.3890
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0062	0.0061	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0120	0.1428	7.0040
Pancreas	0.0027	0.0068	0.3965	2.5219
Penis	0.0000	0.0000	undef	undef
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0021	3.0709	0.3256
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0035			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0111	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0065
Lung	0.0071	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0164
Kidney	0.0247	Lung	0.0070
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 41

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0096	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 42

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000 undef	
Breast	0.0000	0.0019	0.0000 undef	
Small intestine	0.0031	0.0000	undef 0.0000	
Ovary	0.0000	0.0130	0.0000 undef	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0000	0.0000	undef undef	
Brain	0.0037	0.0010	3.5998 0.2778	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0021	0.0000	undef 0.0000	
Heart	0.0058	0.0000	undef 0.0000	
Testicles	0.0052	0.0000	undef 0.0000	
Lung	0.0000	0.0000	undef undef	
Stomach-esophagus	0.0034	0.0000	undef 0.0000	
Muscle-skeleton	0.0000	0.0068	0.0000 undef	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0060	0.0000	undef 0.0000	
Penis	0.0022	0.0000	undef 0.0000	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0064			
Uterus-general	0.0059			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0010
Prostate	0.0499	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 43

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0130	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0235			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 44

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0260	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 45

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000	undef
Breast	0.0090	0.0056	1.5879	0.6298
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0231	0.0828	12.0723
Brain	0.0000	0.0031	0.0000	undef
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0847	0.0433	23.0839
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0021	0.0102	0.2032	4.9209
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0000	0.0110	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0065	0.0000	undef	0.0000
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0491
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 46

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0090	0.0263	0.3403	2.9389
Small intestine	0.0184	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0170	0.0050	3.3962	0.2944
Gastrointestinal	0.0172	0.0046	3.7275	0.2683
Brain	0.0081	0.0216	0.3771	2.6517
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0117	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0020	4.0643	0.2460
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0017	0.0110	0.1496	6.6857
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0043			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0012
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0171
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0000
Placenta	0.0121	Nerves	0.0137
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 47

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0090	0.0019	4.7637	0.2099
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0052	0.0041	1.2701	0.7873
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0180	0.0952	10.5060
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0083	0.0055	1.4957	0.6686
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0107	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0077
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 48

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0026	6.1018	0.1639
Breast	0.0179	0.0169	1.0586	0.9446
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0060	0.0286	0.2093	4.7774
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0287	0.0278	1.0354	0.9658
Brain	0.0229	0.0164	1.3949	0.7169
Hematopoietic	0.0107	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0350	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0239	0.0225	1.0623	0.9414
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0050	0.0000	undef	0.0000
Penis	0.0210	0.0000	undef	0.0000
Prostate	0.0262	0.0085	3.0709	0.3256
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0068	3.3668	0.2970
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0160			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0356			
Sensory organs	0.0000			
White blood cells	0.0208			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0167	Ovary_n	0.1595
Brain	0.0188	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0320	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0077
Kidney	0.0124	Lung	0.0164
Placenta	0.0182	Nerves	0.0221
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0155
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 49

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0057	0.0139	0.4142	2.4145
Brain	0.0037	0.0062	0.6000	1.6668
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0275	0.1542	6.4853
Heart	0.0115	0.0000	undef	0.0000
Testicles	0.0021	0.0041	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0109	0.0137	0.7930	1.2610
Kidney	0.0066	0.0055	1.1966	0.8357
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0044	0.0064	0.6824	1.4654
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0208			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0000			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0000	Ovary_t 0.0000
Hematopoietic 0.0000	Endocrine tissue 0.0000
Skin 0.0039	Fetal 0.0000
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0260	Hematopoietic 0.0065
Lung 0.0000	Skin-muscle 0.0000
Suprarenal gland 0.0036	Testicles 0.0000
Kidney 0.0000	Lung 0.0020
Placenta 0.0000	Nerves 0.0205
Prostate 0.0061	Prostate 0.0000
Sensory organs 0.0000	Sensory Organs 0.0042
	Uterus_n



Electronic Northern for SEQ. ID NO.: 50

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0179	0.4358	2.2944
Breast	0.0064	0.0094	0.6805	1.4694
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0051	0.0075	0.6792	1.4722
Gastrointestinal	0.0057	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0080	0.0379	0.2117	4.7230
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0064	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0073	0.0102	0.7112	1.4060
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0027	0.0137	0.1983	5.0439
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0272	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0087
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0194
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0100
Placenta	0.0061	Nerves	0.0000
Prostate	0.0000	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 51

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0119	0.0075	1.5849	0.6309
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0037	0.0072	0.5143	1.9446
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0074	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0062	0.0061	1.0161	0.9842
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0188	0.0060	3.1411	0.3184
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0153	0.0106	1.4331	0.6978
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0153	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0026			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0052
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0456
Lung	0.0213	Skin-muscle	0.0065
Suprarenal gland	0.0072	Testicles	0.0077
Kidney	0.1014	Lung	0.0164
Placenta	0.0000	Nerves	0.0040
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 52

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0179	0.0038	4.7637	0.2099
Small intestine	0.0092	0.0496	0.1854	5.3946
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0153	0.0251	0.6113	1.6358
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0155	0.0103	1.5119	0.6614
Hematopoietic	0.0040	0.0758	0.0529	18.8919
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0388	0.0000	undef
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0177	0.0143	1.2338	0.8105
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0109	0.0274	0.3965	2.5219
Pancreas	0.0231	0.0221	1.0470	0.9551
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0204	0.3741	2.6732
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0095			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0000
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0023
Hepatic	Gastrointestinal 0.0122
Heart-blood vessels	Hematopoietic 0.0057
Lung	Skin-muscle 0.0000
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0164
Placenta	Nerves 0.0060
Prostate	Nerves 0.0068
Sensory organs	Prostate 0.0000
	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 53

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0153	1.5254	0.6555
Breast	0.0115	0.0113	1.0208	0.9796
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0090	0.0286	0.3140	3.1849
Endocrine tissue	0.0102	0.0125	0.8151	1.2268
Gastrointestinal	0.0230	0.0278	0.8283	1.2072
Brain	0.0148	0.0144	1.0285	0.9723
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0106	0.0275	0.3855	2.5941
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0125	0.0123	1.0161	0.9842
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0137	0.0120	1.1422	0.8755
Kidney	0.0136	0.0274	0.4956	2.0176
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0192	0.5687	1.7585
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0087			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0083	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Endocrine tissue	0.0017
Hepatic	0.0520	Fetal	0.0000
Heart-blood vessels	0.0036	Gastrointestinal	0.0000
Lung	0.0181	Hematopoietic	0.0000
Suprarenal gland	0.0000	Skin-muscle	0.0000
Kidney	0.0371	Testicles	0.0000
Placenta	0.0061	Lung	0.0020
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0126	Prostate	0.0000
		Sensory Organs	
		Uterus n	

Electronic Northern for SEQ. ID NO.: 54

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0052	0.0051	1.0079	0.9921
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0032	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0031	0.0020	1.5241	0.6561
Lung	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0017	0.0060	0.2856	3.5020
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0221	0.0748	13.3713
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0043	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0032			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0000
Suprarenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000
	Breast 0.0068
	Ovary_n 0.0000
	Ovary_t 0.0000
	Endocrine tissue 0.0000
	Fetal 0.0082
	Gastrointestinal 0.0122
	Hematopoietic 0.0114
	Skin-muscle 0.0000
	Testicles 0.0000
	Lung 0.0164
	Nerves 0.0060
	Prostate 0.0068
	Sensory Organs 0.0000
	Uterus_n 0.0083

Electronic Northern for SEQ. ID NO.: 55

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0204	0.1907	5.2444
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0061	0.0496	0.1236	8.0920
Ovary	0.0120	0.0364	0.3289	3.0402
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0046	2.0708	0.4829
Brain	0.0140	0.0185	0.7600	1.3159
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0294	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0138	0.0412	0.3341	2.9932
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0156	0.0164	0.9526	1.0498
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0174	0.0234	0.7445	1.3433
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0139			
Cervix	0.0106			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0304
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0047
Hepatic	Gastrointestinal 0.0488
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0162
Suprarenal gland	Testicles 0.0000
Kidney	Lung 0.0082
Placenta	Nerves 0.0090
Prostate	Prostate 0.0068
Sensory organs	Sensory Organs 0.0000
	Uterus_n 0.0250

Electronic Northern for SEQ. ID NO.: 56

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0153	0.5085	1.9666
Breast	0.0077	0.0132	0.5833	1.7144
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0085	0.0025	3.3962	0.2944
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0072	0.3086	3.2409
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0000	0.0468	0.0000	undef
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0193	0.0153	1.2605	0.7933
Muscle-skeleton	0.0120	0.0120	0.9994	1.0006
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0085	0.7677	1.3026
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0182			
Cervix	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0068
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0028	Ovary_t 0.0152
Hematopoietic 0.0063	Endocrine tissue 0.0245
Skin 0.0039	Fetal 0.0012
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0000
Lung 0.0178	Skin-muscle 0.0065
Suprarenal gland 0.0108	Testicles 0.0000
Kidney 0.0000	Lung 0.0246
Placenta 0.0124	Nerves 0.0060
Prostate 0.0061	Prostate 0.0000
Sensory organs 0.0000	Sensory Organs 0.0042
	Uterus_n

Electronic Northern for SEQ. ID NO.: 57

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0128	0.0150	0.8507	1.1756
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0051	0.0226	0.2264	4.4166
Gastrointestinal	0.0077	0.0000	undef	0.0000
Brain	0.0074	0.0103	0.7200	1.3890
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0085	0.0275	0.3084	3.2426
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0062	0.0102	0.6096	1.6403
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0120	0.0060	1.9989	0.5003
Kidney	0.0217	0.0068	3.1722	0.3152
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0044	0.0085	0.5118	1.9538
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0139			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0068
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0188	Ovary_t	0.0051
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0076
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0124	Lung	0.0082
Placenta	0.0000	Nerves	0.0120
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000



Electronic Northern for SEQ. ID NO.: 58

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0585	0.0332	1.7601	0.5681
Breast	0.0230	0.0132	1.7499	0.5715
Small intestine	0.0153	0.0827	0.1854	5.3946
Ovary	0.0150	0.0546	0.2741	3.6482
Endocrine tissue	0.0136	0.0150	0.9057	1.1042
Gastrointestinal	0.0192	0.0416	0.4602	2.1730
Brain	0.0163	0.0277	0.5866	1.7046
Hematopoietic	0.0374	0.0379	0.9881	1.0121
Skin	0.0404	0.0847	0.4765	2.0985
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0297	0.0412	0.7196	1.3897
Testicles	0.0863	0.1169	0.7380	1.3551
Lung	0.0364	0.0266	1.3678	0.7311
Stomach-esophagus	0.0290	0.0767	0.3782	2.6444
Muscle-skeleton	0.0411	0.0360	1.1422	0.8755
Kidney	0.0190	0.0137	1.3878	0.7206
Pancreas	0.0132	0.0497	0.2659	3.7607
Penis	0.0359	0.0800	0.4493	2.2259
Prostate	0.0262	0.0128	2.0473	0.4885
Uterus-endometrium	0.0338	0.0528	0.6402	1.5621
Uterus-myometrium	0.0229	0.0000	undef	0.0000
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0251			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0528	Ovary_n	0.0000
Brain	0.1189	Ovary_t	0.0000
Hematopoietic	0.0275	Endocrine tissue	0.0093
Skin	0.0000	Fetal	0.0366
Hepatic	0.0520	Gastrointestinal	0.0057
Heart-blood vessels	0.0818	Hematopoietic	0.0389
Lung	0.0253	Skin-muscle	0.0154
Suprarenal gland	0.0254	Testicles	0.0491
Kidney	0.0371	Lung	0.0120
Placenta	0.0424	Nerves	0.0068
Prostate	0.0499	Prostate	0.0077
Sensory organs	0.0251	Sensory Organs	0.0250
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 59

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0056	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0390	0.1535	6.5146
Endocrine tissue	0.0102	0.0251	0.4075	2.4537
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0140	0.0082	1.7099	0.5848
Hematopoietic	0.0053	0.1515	0.0353	28.3379
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0104	0.0184	0.5645	1.7715
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0099	0.0110	0.8974	1.1143
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0022	0.0043	0.5118	1.9538
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0068	0.0000	undef
Uterus-general	0.0192	0.0000	undef	undef
Breast hyperplasia	0.0119			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0118			
Sensory organs	0.0061			
White blood cells	0.0213			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0835	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0375	Ovary_t	0.0203
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0213	Hematopoietic	0.0000
Lung	0.0108	Skin-muscle	0.0162
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0182	Nerves	0.0241
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 63

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0230	0.0000	undef
Breast	0.0000	0.0150	0.0000	undef
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0153	0.0139	1.1045	0.9054
Brain	0.0022	0.0154	0.1440	6.9448
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0064	0.0323	0.0000	undef
Heart	0.0000	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0020	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	6.3239	0.7179	8.8087	0.1135
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000		
Uterus-general	0.0089			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0106			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.2721	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0354
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0017
Hepatic	0.0000	Gastrointestinal	0.2685
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 65

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0064	0.0075	0.8507	1.1756
Small intestine	0.0245	0.0165	1.4830	0.6743
Ovary	0.0090	0.0520	0.1727	5.7908
Endocrine tissue	0.0085	0.0000	undef	0.0000
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0044	0.0123	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0381	0.0970	0.3922	2.5500
Heart	0.0074	0.0137	0.5397	1.8529
Testicles	0.0000	0.0000	undef	undef
Lung	0.0052	0.0082	0.6350	1.5747
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0163	0.0616	0.2643	3.7829
Pancreas	0.0396	0.0055	7.1795	0.1393
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0153	0.2863	0.0534	18.7357
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0043			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0222	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0228
Lung	0.0036	Skin-muscle	0.0162
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0082
Placenta	0.0242	Nerves	0.0010
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 67

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0102	0.3814	2.6222
Breast	0.0026	0.0169	0.1512	6.6125
Small intestine	0.0092	0.0165	0.5561	1.7982
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0057	0.0185	0.3106	3.2193
Brain	0.0044	0.0062	0.7200	1.3890
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0031	0.0102	0.3048	3.2806
Stomach-esophagus	0.0097	0.0153	0.6303	1.5866
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0081	0.0068	1.1896	0.8406
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0022	0.0085	0.2559	3.9077
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	0.0272
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0245
Skin	0.0157	Fetal	0.0169
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0171
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0328
Placenta	0.0121	Nerves	0.0080
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 69

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0038	0.0000	undef	0.0000
Brain	0.0007	0.0021	0.3600	2.7779
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0288	0.0000	undef	0.0000
Lung	0.0031	0.0000	undef	0.0000
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0054	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0017	0.0954	0.1067	9.3678
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0000	Ovary_t	0.0152
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0342
Lung	0.0000	Skin-muscle	0.0097
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0020
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 70

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0060	0.0260	0.2303	4.3431
Endocrine tissue	0.0324	0.0075	4.3019	0.2325
Gastrointestinal	0.0134	0.0093	1.4496	0.6898
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0379	0.1059	9.4460
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0148	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0135	0.0102	1.3209	0.7571
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0060	0.2856	3.5020
Kidney	0.0109	0.0068	1.5861	0.6305
Pancreas	0.0099	0.0055	1.7949	0.5571
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0109	0.0085	1.2795	0.7815
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0130			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0041
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0142	Hematopoietic	0.0057
Lung	0.0072	Skin-muscle	0.0097
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0182	Nerves	0.0070
Prostate	0.0249	Prostate	0.0137
Sensory organs	0.0126	Sensory Organs	0.0000
		Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 72

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.0895	1.1768	0.8498
Breast	0.0652	0.0846	0.7713	1.2966
Small intestine	0.1073	0.0992	1.0813	0.9248
Ovary	0.0629	0.1353	0.4649	2.1509
Endocrine tissue	0.0579	0.0451	1.2830	0.7794
Gastrointestinal	0.1379	0.2220	0.6213	1.6096
Brain	0.0702	0.0534	1.3153	0.7603
Hematopoietic	0.1056	0.1136	0.9293	1.0761
Skin	0.0587	0.0847	0.6931	1.4427
Hepatic	0.0285	0.1035	0.2757	3.6266
Heart	0.1293	0.0412	3.1353	0.3189
Testicles	0.0403	0.1754	0.2296	4.3556
Lung	0.0914	0.1063	0.8598	1.1631
Stomach-esophagus	0.0387	0.1840	0.2101	4.7599
Muscle-skeleton	0.0548	0.1260	0.4351	2.2982
Kidney	0.0814	0.1438	0.5665	1.7654
Pancreas	0.0363	0.1878	0.1936	5.1662
Penis	0.1138	0.0800	1.4227	0.7029
Prostate	0.0697	0.0958	0.7279	1.3738
Uterus-endometrium	0.1824	0.0000	undef	0.0000
Uterus-myometrium	0.0838	0.0951	0.8818	1.1341
Uterus-general	0.1171	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0922			
Seminal vesicle	0.0712			
Sensory organs	0.0706			
White blood cells	0.1448			
Cervix	0.1810			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0557	Breast	0.0340
Gastrointestinal	0.1083	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0253
Hematopoietic	0.0944	Endocrine tissue	0.0000
Skin	0.2513	Fetal	0.0163
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0712	Hematopoietic	0.0000
Lung	0.1409	Skin-muscle	0.0292
Suprarenal gland	0.0507	Testicles	0.0077
Kidney	0.1297	Lung	0.0246
Kidney	0.0545	Nerves	0.0090
Placenta	0.0499	Prostate	0.0274
Prostate	0.0251	Prostate	0.0000
Sensory organs		Sensory Organs	0.0042
		Uterus n	



Electronic Northern for SEQ. ID NO.: 73

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0895	0.7409	1.3497
Breast	0.0371	0.0489	0.7591	1.3174
Small intestine	0.0766	0.0000	undef	0.0000
Ovary	0.0270	0.0754	0.3573	2.7989
Endocrine tissue	0.0170	0.0326	0.5225	1.9139
Gastrointestinal	0.0805	0.0833	0.9664	1.0348
Brain	0.0177	0.0390	0.4547	2.1992
Hematopoietic	0.0896	0.0758	1.1822	0.8459
Skin	0.0551	0.1695	0.3249	3.0779
Hepatic	0.0238	0.0776	0.3064	3.2640
Heart	0.0604	0.1237	0.4883	2.0480
Testicles	0.0298	0.0702	0.4100	2.4391
Lung	0.0519	0.0429	1.2096	0.8267
Stomach-esophagus	0.0676	0.0843	0.8022	1.2466
Muscle-skeleton	0.0223	0.0240	0.9280	1.0775
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0132	0.0773	0.1709	5.8500
Penis	0.0838	0.0533	1.5724	0.6360
Prostate	0.0567	0.0255	2.2179	0.4509
Uterus-endometrium	0.0946	0.0000	undef	0.0000
Uterus-myometrium	0.0762	0.0679	1.1223	0.8911
Uterus-general	0.0407	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0445			
Sensory organs	0.0235			
White blood cells	0.0772			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0272
Gastrointestinal	0.0305	Ovary_n	0.0000
Brain	0.0313	Ovary_t	0.1468
Hematopoietic	0.0393	Endocrine tissue	0.0245
Skin	0.0000	Fetal	0.0105
Hepatic	0.0260	Gastrointestinal	0.0366
Heart-blood vessels	0.0285	Hematopoietic	0.0057
Lung	0.0145	Skin-muscle	0.0292
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0679	Lung	0.0328
Placenta	0.0364	Nerves	0.0040
Prostate	0.0997	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 74

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0468	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0110	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0353	0.0164	2.1591	0.4631
Lung	0.1836	0.1227	1.4969	0.6681
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0050	0.0221	0.2244	4.4571
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0022	0.0128	0.1706	5.8615
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000			
Uterus-general	0.1246			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 76

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0077	0.0000	undef
Breast	0.0026	0.0301	0.0851	11.7556
Small intestine	0.0000	0.0331	0.0000	undef
Ovary	0.0030	0.0728	0.0411	24.3213
Endocrine tissue	0.0000	0.0100	0.0000	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0510	0.0596	0.8565	1.1675
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0037	0.1695	0.0217	46.1678
Hepatic	0.0523	0.1747	0.2996	3.3382
Heart	0.0138	0.0137	1.0023	0.9977
Testicles	0.0000	0.0935	0.0000	undef
Lung	0.0073	0.0818	0.0889	11.2478
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0240	0.2760	0.0869	11.5066
Kidney	0.3910	0.4108	0.9516	1.0508
Pancreas	0.1123	0.0387	2.9060	0.3441
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.2111	0.0320	31.2422
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.1838			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0696	Breast	0.0000
Gastrointestinal	0.0194	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0128
Hepatic	0.0107	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0000
Lung	0.0254	Skin-muscle	0.0032
Suprarenal gland	0.0062	Testicles	0.0000
Kidney	0.2302	Lung	0.0164
Placenta	0.0000	Nerves	0.0231
Prostate	0.1632	Prostate	0.0068
Sensory organs		Sensory Organs	0.0310
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 78

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0153	1.0170	0.9833
Breast	0.0090	0.0244	0.3664	2.7290
Small intestine	0.0123	0.0496	0.2472	4.0460
Ovary	0.0090	0.0338	0.2657	3.7640
Endocrine tissue	0.0136	0.0226	0.6038	1.6562
Gastrointestinal	0.0172	0.0324	0.5325	1.8779
Brain	0.0044	0.0216	0.2057	4.8614
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0000	0.0000	undef	undef
Lung	0.0073	0.0286	0.2540	3.9367
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0051	0.0180	0.2856	3.5020
Kidney	0.0190	0.0068	2.7756	0.3603
Pancreas	0.0083	0.0110	0.7479	1.3371
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0131	0.0106	1.2284	0.8141
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0136	0.5611	1.7821
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0113			
Cervix	0.0213			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0250	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0152
Hematopoietic	0.0118	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0256
Hepatic	0.0260	Gastrointestinal	0.0122
Heart-blood vessels	0.0178	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0309
Kidney	0.0371	Lung	0.0164
Placenta	0.0061	Nerves	0.0100
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0377	Sensory Organs	0.1084
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 79

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0273	0.0332	0.8214	1.2174
Breast	0.0230	0.0188	1.2250	0.8164
Small intestine	0.0276	0.0331	0.8342	1.1988
Ovary	0.0210	0.0650	0.3224	3.1022
Endocrine tissue	0.0238	0.0276	0.8645	1.1567
Gastrointestinal	0.0172	0.0463	0.3728	2.6827
Brain	0.0118	0.0144	0.8228	1.2153
Hematopoietic	0.0214	0.0379	0.5646	1.7711
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0540	0.0550	0.9830	1.0173
Testicles	0.0173	0.0585	0.2952	3.3877
Lung	0.0322	0.0450	0.7159	1.3969
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0240	0.0600	0.3998	2.5014
Kidney	0.0353	0.0548	0.6443	1.5520
Pancreas	0.0165	0.0221	0.7479	1.3371
Penis	0.0150	0.0267	0.5616	1.7807
Prostate	0.0240	0.0405	0.5926	1.6874
Uterus-endometrium	0.0270	0.1055	0.2561	3.9053
Uterus-myometrium	0.0381	0.0068	5.6113	0.1782
Uterus-general	0.0051	0.1908	0.0267	37.4714
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0534			
Sensory organs	0.0588			
White blood cells	0.0234			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	0.0557	Breast 0.0136
Gastrointestinal	0.0083	Ovary_n 0.0000
Brain	0.0063	Ovary_t 0.0051
Hematopoietic	0.0039	Endocrine tissue 0.0245
Skin	0.0000	Fetal 0.0256
Hepatic	0.0000	Gastrointestinal 0.0122
Heart-blood vessels	0.0142	Hematopoietic 0.0000
Lung	0.0253	Skin-muscle 0.0583
Suprarenal gland	0.0507	Testicles 0.0231
Kidney	0.0432	Lung 0.0491
Placenta	0.0303	Nerves 0.0221
Prostate	0.1247	Prostate 0.0821
Sensory organs	0.0251	Sensory Organs 0.0000
		Uterus_n 0.0416

Electronic Northern for SEQ. ID NO.: 80

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0000	undef	0.0000
Breast	0.0026	0.0075	0.3403	2.9389
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0017	0.0025	0.6792	1.4722
Gastrointestinal	0.0000	0.0139	0.0000	undef
Brain	0.0044	0.0041	1.0799	0.9260
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0058	0.0117	0.4920	2.0326
Testicles	0.0010	0.0020	0.5080	1.9684
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0054	0.0000	undef	0.0000
Kidney	0.0033	0.0055	0.5983	1.6714
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0044	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0068	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0064			
Breast hyperplasia	0.0059			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0017			
White blood cells	0.0106			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal	Ovary_n 0.0000
Brain	Ovary_t 0.0051
Hematopoietic	Endocrine tissue 0.0000
Skin	Fetal 0.0093
Hepatic	Gastrointestinal 0.0000
Heart-blood vessels	Hematopoietic 0.0114
Lung	Skin-muscle 0.0309
Suprarenal gland	Testicles 0.0082
Kidney	Lung 0.0060
Placenta	Nerves 0.0068
Prostate	Prostate 0.0000
Sensory organs	Sensory Organs 0.0000
	Uterus_n

Electronic Northern for SEQ. ID NO.: 81

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0141	0.0150	0.9357	1.0687
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0090	0.0416	0.2159	4.6326
Endocrine tissue	0.0119	0.0176	0.6792	1.4722
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0126	0.0031	4.0798	0.2451
Hematopoietic	0.0080	0.1136	0.0706	14.1689
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0065	0.7353	1.3600
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0104	0.0164	0.6350	1.5747
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0120	0.5711	1.7510
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0131	0.0021	6.1418	0.1628
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0136	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS		STANDARDIZED/SUBTRACTED
	% frequency		LIBRARIES
			% frequency
Development	0.0278	Breast	0.0000
Gastrointestinal	0.0111	Ovary_n	0.1595
Brain	0.0250	Ovary_t	0.0152
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0285	Hematopoietic	0.0057
Lung	0.0108	Skin-muscle	0.0065
Suprarenal gland	0.0254	Testicles	0.0231
Kidney	0.0000	Lung	0.0082
Placenta	0.0000	Nerves	0.0191
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0377	Sensory Organs	0.0155
		Uterus_n	0.0250

Electronic Northern for SEQ. ID NO.: 82

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0351	0.0435	0.8076	1.2383
Small intestine	0.0576	0.0489	1.1778	0.8490
Ovary	0.0337	0.0165	2.0391	0.4904
Endocrine tissue	0.0659	0.1353	0.4871	2.0531
Gastrointestinal	0.0801	0.0878	0.9121	1.0963
Brain	0.0441	0.1203	0.3664	2.7294
Hematopoietic	0.1072	0.0298	3.5998	0.2778
Skin	0.0201	0.1515	0.1323	7.5568
Hepatic	0.0661	0.0000	undef	0.0000
Heart	0.0428	0.0582	0.7353	1.3600
Testicles	0.0572	0.0687	0.8327	1.2010
Lung	0.0460	0.1988	0.2315	4.3193
Stomach-esophagus	0.0416	0.0634	0.6555	1.5255
Muscle-skeleton	0.0290	0.0613	0.4727	2.1155
Kidney	0.0360	0.0180	1.9989	0.5003
Pancreas	0.0489	0.0411	1.1896	0.8406
Penis	0.1371	0.0552	2.4829	0.4028
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0741	0.0426	1.7402	0.5747
Uterus-myometrium	0.0203	0.0000	undef	0.0000
Uterus-general	0.0534	0.0475	1.1223	0.8911
Breast hyperplasia	0.0407	0.0000	undef	0.0000
Prostate hyperplasia	0.0639			
Seminal vesicle	0.0476			
Sensory organs	0.0623			
White blood cells	0.0588			
Cervix	0.0546			
	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development		Breast	
Gastrointestinal	0.0696	Ovary_n	0.0068
Brain	0.1971	Ovary_t	0.0000
Hematopoietic	0.0500	Endocrine tissue	0.0304
Skin	0.0551	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0262
Heart-blood vessels	0.1040	Hematopoietic	0.1220
Lung	0.0427	Skin-muscle	0.0285
Suprarenal gland	0.1120	Testicles	0.0356
Kidney	0.1521	Lung	0.0309
Placenta	0.0309	Nerves	0.2211
Prostate	0.1212	Prostate	0.0502
Sensory organs	0.0748	Sensory Organs	0.0615
	0.0628	Uterus n	0.1471
			0.0125



Electronic Northern for SEQ. ID NO.: 83

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0156	0.0077	2.0339	0.4917
Breast	0.0307	0.0169	1.8147	0.5510
Small intestine	0.0123	0.0165	0.7415	1.3487
Ovary	0.0120	0.0416	0.2878	3.4745
Endocrine tissue	0.0273	0.0176	1.5526	0.6441
Gastrointestinal	0.0153	0.0324	0.4733	2.1127
Brain	0.0192	0.0154	1.2479	0.8013
Hematopoietic	0.0147	0.0379	0.3882	2.5762
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0238	0.0065	3.6765	0.2720
Heart	0.0170	0.0137	1.2336	0.8107
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0177	0.0204	0.8637	1.1579
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0154	0.0060	2.5700	0.3891
Kidney	0.0190	0.0000	undef	0.0000
Pancreas	0.0132	0.0166	0.7977	1.2536
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0109	0.0106	1.0236	0.9769
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.0000	undef	0.0000
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0416			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0178			
Sensory organs	0.0235			
White blood cells	0.0087			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0068
Gastrointestinal	0.0278	Ovary_n	0.1595
Brain	0.0056	Ovary_t	0.0051
Hematopoietic	0.0438	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0427	Skin-muscle	0.0097
Suprarenal gland	0.0145	Testicles	0.0000
Kidney	0.0254	Lung	0.0491
Placenta	0.0062	Nerves	0.0231
Prostate	0.0000	Prostate	0.0342
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0377	Uterus_n	0.0083

Electronic Northern for SEQ. ID NO.: 84

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0153	2.0339	0.4917
Breast	0.0192	0.0320	0.6005	1.6654
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0060	0.0416	0.1439	6.9489
Endocrine tissue	0.0273	0.0451	0.6038	1.6562
Gastrointestinal	0.0230	0.0093	2.4850	0.4024
Brain	0.0177	0.0164	1.0799	0.9260
Hematopoietic	0.0174	0.0379	0.4587	2.1798
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0381	0.0065	5.8824	0.1700
Heart	0.0159	0.0000	undef	0.0000
Testicles	0.0115	0.0351	0.3280	3.0489
Lung	0.0187	0.0123	1.5241	0.6561
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0109	0.0205	0.5287	1.8915
Pancreas	0.0083	0.0166	0.4986	2.0057
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0131	0.0064	2.0473	0.4885
Uterus-endometrium	0.0405	0.0528	0.7682	1.3018
Uterus-myometrium	0.0305	0.0204	1.4964	0.6683
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0327			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0165			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0272
Gastrointestinal 0.0557	Ovary_n 0.0000
Brain 0.0222	Ovary_t 0.0152
Hematopoietic 0.0250	Endocrine tissue 0.0000
Skin 0.0118	Fetal 0.0000
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0259
Lung 0.0249	Skin-muscle 0.0000
Suprarenal gland 0.0181	Testicles 0.0246
Kidney 0.0000	Lung 0.0341
Placenta 0.0062	Nerves 0.0274
Prostate 0.0242	Prostate 0.0000
Sensory organs 0.0249	Sensory Organs 0.0125
	Uterus_n

Electronic Northern for SEQ. ID NO.: 85

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0102	0.0000 undef	
Breast	0.0051	0.0395	0.1296 7.7146	
Small intestine	0.0092	0.0165	0.5561 1.7982	
Ovary	0.0030	0.0312	0.0959 10.4234	
Endocrine tissue	0.0000	0.0050	0.0000 undef	
Gastrointestinal	0.0038	0.0139	0.2761 3.6217	
Brain	0.0081	0.0113	0.7200 1.3890	
Hematopoietic	0.0027	0.0000	undef 0.0000	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0000	0.0000	undef undef	
Heart	0.0074	0.0000	undef 0.0000	
Testicles	0.0000	0.0117	0.0000 undef	
Lung	0.0062	0.0020	3.0482 0.3281	
Stomach-esophagus	0.0097	0.0077	1.2605 0.7933	
Muscle-skeleton	0.0034	0.0120	0.2856 3.5020	
Kidney	0.0027	0.0000	undef 0.0000	
Pancreas	0.0033	0.0000	undef 0.0000	
Penis	0.0030	0.1066	0.0281 35.6140	
Prostate	0.0044	0.0043	1.0236 0.9769	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0076	0.0000	undef 0.0000	
Uterus-general	0.0153	0.0000	undef 0.0000	
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0026			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0087
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0000	Skin-muscle	0.0057
Suprarenal gland	0.0000	Testicles	0.0032
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0082
Prostate	0.0000	Prostate	0.0010
Sensory organs	0.0000	Sensory Organs	0.0068
		Uterus_n	0.0000
			0.0333

Electronic Northern for SEQ. ID NO.: 88

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0486	0.4014	2.4911
Breast	0.0064	0.0338	0.1890	5.2900
Small intestine	0.0153	0.0165	0.9268	1.0789
Ovary	0.0030	0.0182	0.1645	6.0803
Endocrine tissue	0.0136	0.0000	undef	0.0000
Gastrointestinal	0.0134	0.0139	0.9664	1.0348
Brain	0.0052	0.0123	0.4200	2.3811
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0184	0.0847	0.2166	4.6168
Hepatic	0.0048	0.0388	0.1225	8.1599
Heart	0.0074	0.0962	0.0771	12.9706
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0665	0.0573	1.1612	0.8612
Stomach-esophagus	0.0193	0.0383	0.5042	1.9833
Muscle-skeleton	0.0788	0.0300	2.6271	0.3807
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0116	0.0166	0.6980	1.4326
Penis	0.0000	0.0800	0.0000	undef
Prostate	0.0065	0.0106	0.6142	1.6282
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0954	0.0000	undef
Uterus-general	0.0128			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.1682			
White blood cells	0.0000			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0557
Hematopoietic	0.0111	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0039	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0062	Nerves	0.0000
Prostate	0.0364	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
	0.0000	Uterus_n	

Electronic Northern for SEQ. ID NO.: 89

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0128	0.3051	3.2777
Breast	0.0153	0.0038	4.0832	0.2449
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0068	0.0025	2.7170	0.3681
Gastrointestinal	0.0077	0.0046	1.6567	0.6036
Brain	0.0052	0.0021	2.5199	0.3968
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0844	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0201	0.0275	0.7324	1.3653
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0156	0.0061	2.5402	0.3937
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0050	0.0055	0.8974	1.1143
Penis	0.0329	0.1066	0.3089	3.2376
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0032	0.0000	undef	undef
Uterus-general	0.0030			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0121			
Sensory organs	0.0852			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0087
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0107	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0020
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0125

Electronic Northern for SEQ. ID NO.: 90

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0038	0.0169	0.2268	4.4083
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0051	0.0326	0.1567	6.3796
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0067	0.0062	1.0799	0.9260
Hematopoietic	0.0080	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0201	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0083	0.0143	0.5806	1.7223
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0109	0.0137	0.7930	1.2610
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0356			
Sensory organs	0.0118			
White blood cells	0.0052			
Cervix	0.0000			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0111	Ovary_t 0.0000
Hematopoietic 0.0125	Endocrine tissue 0.0000
Skin 0.0118	Fetal 0.0064
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0057
Lung 0.0107	Skin-muscle 0.0130
Suprarenal gland 0.0181	Testicles 0.0231
Kidney 0.0000	Lung 0.0164
Placenta 0.0124	Nerves 0.0060
Prostate 0.0061	Prostate 0.0137
Sensory organs 0.0000	Sensory Organs 0.0000
	Uterus_n 0.0042

Electronic Northern for SEQ. ID NO.: 91

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0051	0.0094	0.5444	1.8368
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0119	0.0150	0.7925	1.2619
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0081	0.0082	0.9899	1.0102
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0127	0.0412	0.3084	3.2426
Testicles	0.0173	0.0000	undef	0.0000
Lung	0.0073	0.0307	0.2371	4.2179
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0033	0.0166	0.1994	5.0142
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0000	0.0106	0.0000	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0035			
Cervix	0.0106			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	% frequency
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0079	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0064
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0071	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0328
Placenta	0.0121	Nerves	0.0040
Prostate	0.0000	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0083

Electronic Northern for SEQ. ID NO.: 92

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0038	0.0132	0.2917 3.4287	
Small intestine	0.0031	0.0165	0.1854 5.3946	
Ovary	0.0000	0.0182	0.0000 undef	
Endocrine tissue	0.0051	0.0075	0.6792 1.4722	
Gastrointestinal	0.0038	0.0000	undef 0.0000	
Brain	0.0015	0.0000	undef 0.0000	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0073	0.0000	undef 0.0000	
Hepatic	0.0048	0.0000	undef 0.0000	
Heart	0.0011	0.0137	0.0771 12.9706	
Testicles	0.0000	0.0000	undef undef	
Lung	0.0145	0.0061	2.3708 0.4218	
Stomach-esophagus	0.0000	0.0153	0.0000 undef	
Muscle-skeleton	0.0017	0.0000	undef 0.0000	
Kidney	0.0054	0.0000	undef 0.0000	
Pancreas	0.0017	0.0000	undef 0.0000	
Penis	0.0030	0.0000	undef 0.0000	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0051	0.0000	undef 0.0000	
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0235			
Sensory organs	0.0139			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0068
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0077
Kidney	0.0000	Lung	0.0164
Placenta	0.0061	Nerves	0.0040
Prostate	0.0000	Nerves	0.0000
Sensory organs	0.0000	Prostate	0.0000
		Sensory Organs	0.0000
		Uterus_n	



Electronic Northern for SEQ. ID NO.: 93

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0153	0.0000	undef
Breast	0.0077	0.0113	0.6805	1.4694
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0286	0.1047	9.5548
Endocrine tissue	0.0034	0.0075	0.4528	2.2083
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0059	0.0082	0.7200	1.3890
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0234	0.4920	2.0326
Lung	0.0021	0.0061	0.3387	2.9526
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0000	undef	0.0000
Kidney	0.0054	0.0068	0.7930	1.2610
Pancreas	0.0017	0.0331	0.0499	20.0570
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0032			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0009			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0245
Skin	0.0039	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0062	Lung	0.0070
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 94

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0115	0.0132	0.8750	1.1429
Small intestine	0.0337	0.0496	0.6797	1.4713
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0085	0.0251	0.3396	2.9444
Gastrointestinal	0.0747	0.0879	0.8501	1.1763
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0048	0.0194	0.2451	4.0800
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0351	0.0000	undef
Lung	0.0042	0.0143	0.2903	3.4446
Stomach-esophagus	0.0483	0.0077	6.3027	0.1587
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0163	0.0137	1.1896	0.8406
Pancreas	0.0231	0.0166	1.3960	0.7163
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064			
Uterus-general	0.0119			
Breast hyperplasia	0.0089			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0106			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0108	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0124	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 95

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1092	0.0460	2.3729	0.4214
Breast	0.0627	0.0865	0.7249	1.3795
Small intestine	0.1012	0.1158	0.8739	1.1443
Ovary	0.0599	0.1509	0.3970	2.5190
Endocrine tissue	0.0852	0.2984	0.2854	3.5039
Gastrointestinal	0.0900	0.0925	0.9733	1.0274
Brain	0.1811	0.0637	2.8450	0.3515
Hematopoietic	0.0521	0.1136	0.4587	2.1798
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0809	0.0582	1.3889	0.7200
Heart	0.1092	0.0962	1.1344	0.8815
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0634	0.1104	0.5739	1.7425
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0463	0.0420	1.1014	0.9079
Kidney	0.0706	0.1369	0.5155	1.9400
Pancreas	0.0743	0.1049	0.7085	1.4114
Penis	0.1467	0.0800	1.8345	0.5451
Prostate	0.0567	0.0873	0.6491	1.5405
Uterus-endometrium	0.0811	0.0000	undef	0.0000
Uterus-myometrium	0.1067	0.1155	0.9242	1.0820
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.1407			
Prostate hyperplasia	0.0713			
Seminal vesicle	0.0534			
Sensory organs	0.0353			
White blood cells	0.0390			
Cervix	0.0532			

	FETUS	STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0068
Gastrointestinal	0.1113	Ovary_n	0.0000
Brain	0.0694	Ovary_t	0.0253
Hematopoietic	0.0938	Endocrine tissue	0.0000
Skin	0.0590	Fetal	0.0116
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.1281	Skin-muscle	0.0454
Suprarenal gland	0.0397	Testicles	0.0077
Kidney	0.0507	Lung	0.0246
Placenta	0.0432	Nerves	0.0753
Prostate	0.0485	Prostate	0.0205
Sensory organs	0.0499	Sensory Organs	0.0077
	0.1381	Uterus_n	0.0500

Electronic Northern for SEQ. ID NO.: 96

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0013	0.0038	0.3403	2.9389
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0130	0.0000	undef
Endocrine tissue	0.0034	0.0025	1.3585	0.7361
Gastrointestinal	0.0057	0.0093	0.6213	1.6096
Brain	0.0015	0.0041	0.3600	2.7779
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0042	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0061	0.1693	5.9051
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0027	0.0000	undef	0.0000
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0135	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0136	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0030			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0042
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 97

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0102	1.1441	0.8741
Breast	0.0077	0.0075	1.0208	0.9796
Small intestine	0.0061	0.0331	0.1854	5.3946
Ovary	0.0030	0.0390	0.0768	13.0292
Endocrine tissue	0.0051	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0044	0.0154	0.2880	3.4724
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0095	0.0970	0.0980	10.1999
Heart	0.0000	0.0000	undef	undef
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0789	0.0532	1.4850	0.6734
Stomach-esophagus	0.0290	0.0077	3.7816	0.2644
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0120	0.0267	0.4493	2.2259
Prostate	0.0153	0.0021	7.1654	0.1396
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0445			
Sensory organs	0.1411			
White blood cells	0.0026			
Cervix	0.1917			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0340
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0061	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 98

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0000	undef undef	
Breast	0.0013	0.0056	0.2268 4.4083	
Small intestine	0.0092	0.0000	undef 0.0000	
Ovary	0.0000	0.0130	0.0000 undef	
Endocrine tissue	0.0000	0.0000	undef undef	
Gastrointestinal	0.0000	0.0093	0.0000 undef	
Brain	0.0007	0.0021	0.3600 2.7779	
Hematopoietic	0.0000	0.0000	undef undef	
Skin	0.0000	0.0000	undef undef	
Hepatic	0.0095	0.0000	undef 0.0000	
Heart	0.0011	0.0000	undef 0.0000	
Testicles	0.0000	0.0234	0.0000 undef	
Lung	0.0021	0.0020	1.0161 0.9842	
Stomach-esophagus	0.0000	0.0000	undef undef	
Muscle-skeleton	0.0027	0.0000	undef 0.0000	
Kidney	0.0000	0.0000	undef undef	
Pancreas	0.0000	0.0000	undef undef	
Penis	0.0000	0.0000	undef undef	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0000	0.0000	undef undef	
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0017			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0735
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0083
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 99

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0026	1.5254	0.6555
Small intestine	0.0090	0.0056	1.5879	0.6298
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0156	0.0000	undef
Gastrointestinal	0.0051	0.0025	2.0377	0.4907
Brain	0.0019	0.0046	0.4142	2.4145
Hematopoietic	0.0015	0.0041	0.3600	2.7779
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0037	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0074	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0031	0.0000	undef	0.0000
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0103	0.0060	1.7133	0.5837
Pancreas	0.0081	0.0068	1.1896	0.8406
Penis	0.0050	0.0000	undef	0.0000
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0044	0.0064	0.6824	1.4654
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0064			
Seminal vesicle	0.0059			
Sensory organs	0.0089			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0204
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0134
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0097
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0164
Placenta	0.0000	Nerves	0.0100
Prostate	0.0424	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0077
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 100

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0179	1.7434	0.5736
Breast	0.0205	0.0244	0.8376	1.1939
Small intestine	0.0675	0.0000	undef	0.0000
Ovary	0.0060	0.0442	0.1354	7.3832
Endocrine tissue	0.0051	0.0025	2.0377	0.4907
Gastrointestinal	0.0862	0.0463	1.8638	0.5365
Brain	0.0067	0.0133	0.4984	2.0063
Hematopoietic	0.0120	0.0000	undef	0.0000
Skin	0.0477	0.0000	undef	0.0000
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0212	0.0412	0.5140	1.9456
Testicles	0.0230	0.0234	0.9839	1.0163
Lung	0.0374	0.0450	0.8313	1.2029
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0600	0.2284	4.3775
Kidney	0.0054	0.0274	0.1983	5.0439
Pancreas	0.0066	0.0442	0.1496	6.6857
Penis	0.0449	0.0267	1.6847	0.5936
Prostate	0.0240	0.0234	1.0236	0.9769
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0136	1.6834	0.5940
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0384			
Prostate hyperplasia	0.0238			
Seminal vesicle	0.0534			
Sensory organs	0.0235			
White blood cells	0.0303			
Cervix	0.0319			

FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0304
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0064
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0213	Skin-muscle	0.0000
Suprarenal gland	0.0072	Testicles	0.0227
Kidney	0.0000	Lung	0.0309
Placenta	0.0000	Nerves	0.0164
Prostate	0.0182	Prostate	0.0020
Sensory organs	0.0000	Sensory Organs	0.0137
	0.0000	Uterus_n	0.0000
			0.0042



Electronic Northern for SEQ. ID NO.: 101

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0077	0.5085	1.9666
Breast	0.0000	0.0188	0.0000	undef
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0120	0.0442	0.2709	3.6916
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0134	0.0185	0.7248	1.3797
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0321	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0129	0.0000	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0478	0.0450	1.0623	0.9414
Stomach-esophagus	0.0676	0.0690	0.9804	1.0200
Muscle-skeleton	0.0069	0.0000	undef	0.0000
Kidney	0.0000	0.0068	0.0000	undef
Pancreas	0.0116	0.0055	2.0940	0.4775
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0235			
Sensory organs	0.1101			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0082
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 102

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0234	0.0588	0.3979	2.5129
Breast	0.0179	0.0507	0.3529	2.8339
Small intestine	0.0245	0.0000	undef	0.0000
Ovary	0.0180	0.0546	0.3289	3.0402
Endocrine tissue	0.0324	0.0251	1.2906	0.7749
Gastrointestinal	0.0364	0.0786	0.4629	2.1603
Brain	0.0067	0.0216	0.3086	3.2409
Hematopoietic	0.0174	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0048	0.0323	0.1471	6.7999
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0270	0.0225	1.2008	0.8328
Stomach-esophagus	0.0290	0.0383	0.7563	1.3222
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0326	0.0616	0.5287	1.8915
Pancreas	0.0132	0.0607	0.2176	4.5964
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0068	2.2445	0.4455
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0069			
Cervix	0.0106			

	FETUS		STANDARDIZED/SUBTRACTED
	% frequency		LIBRARIES
			% frequency
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0136
Brain	0.0167	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0253
Skin	0.0079	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0169
Heart-blood vessels	0.0000	Hematopoietic	0.0488
Lung	0.0325	Skin-muscle	0.0114
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0231
Placenta	0.0303	Nerves	0.0164
Prostate	0.0249	Prostate	0.0100
Sensory organs	0.0000	Sensory Organs	0.0205
		Uterus_n	0.0077
			0.0083

Electronic Northern for SEQ. ID NO.: 103

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.0256	1.3729	0.7284
Breast	0.0077	0.0094	0.8166	1.2245
Small intestine	0.0153	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0027	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0125	0.0204	0.6096	1.6403
Stomach-esophagus	0.0290	0.0307	0.9454	1.0578
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0066	0.0110	0.5983	1.6714
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0109	0.0170	0.6398	1.5631
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0000	undef	0.0000
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0178			
Seminal vesicle	0.0178			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0272
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0410
Placenta	0.0242	Nerves	0.0010
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 105

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0230	1.3559	0.7375
Breast	0.0435	0.0320	1.3611	0.7347
Small intestine	0.0429	0.0165	2.5952	0.3853
Ovary	0.0210	0.0676	0.3100	3.2263
Endocrine tissue	0.0341	0.0752	0.4528	2.2083
Gastrointestinal	0.0230	0.0185	1.2425	0.8048
Brain	0.0525	0.0554	0.9466	1.0564
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0330	0.0000	undef	0.0000
Hepatic	0.0143	0.0259	0.5515	1.8133
Heart	0.0329	0.0962	0.3414	2.9288
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0166	0.0327	0.5080	1.9684
Stomach-esophagus	0.0193	0.0307	0.6303	1.5866
Muscle-skeleton	0.0343	0.0240	1.4278	0.7004
Kidney	0.0624	0.0822	0.7600	1.3158
Pancreas	0.0182	0.0055	3.2906	0.3039
Penis	0.0419	0.0000	undef	0.0000
Prostate	0.0174	0.0405	0.4310	2.3202
Uterus-endometrium	0.0135	0.1055	0.1280	7.8106
Uterus-myometrium	0.0381	0.0136	2.8057	0.3564
Uterus-general	0.0662	0.0954	0.6939	1.4412
Breast hyperplasia	0.0608			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0623			
Sensory organs	0.0235			
White blood cells	0.0035			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0500	Ovary_t	0.0101
Hematopoietic	0.0876	Endocrine tissue	0.0490
Skin	0.0039	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0142	Skin-muscle	0.0356
Suprarenal gland	0.0434	Testicles	0.0154
Kidney	0.0000	Lung	0.0410
Placenta	0.0556	Nerves	0.0402
Prostate	0.0364	Nerves	0.0205
Sensory organs	0.0000	Prostate	0.0000
	0.1130	Sensory Organs	0.0375
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 106

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0639	0.3051	3.2777
Breast	0.0333	0.0470	0.7077	1.4129
Small intestine	0.0399	0.1819	0.2191	4.5647
Ovary	0.0150	0.0702	0.2132	4.6905
Endocrine tissue	0.0238	0.0903	0.2642	3.7857
Gastrointestinal	0.0900	0.1110	0.8111	1.2329
Brain	0.0067	0.0267	0.2492	4.0126
Hematopoietic	0.0067	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0323	0.4412	2.2666
Heart	0.0011	0.0962	0.0110	90.7941
Testicles	0.0000	0.0234	0.0000	undef
Lung	0.0062	0.0184	0.3387	2.9526
Stomach-esophagus	0.0483	0.3527	0.1370	7.2985
Muscle-skeleton	0.0000	0.0360	0.0000	undef
Kidney	0.0733	0.1575	0.4655	2.1483
Pancreas	0.0694	0.0276	2.5128	0.3980
Penis	0.0090	0.0533	0.1685	5.9357
Prostate	0.0109	0.0255	0.4265	2.3446
Uterus-endometrium	0.0270	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0272	0.2806	3.5642
Uterus-general	0.0000	0.4771	0.0000	undef
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.1068			
Sensory organs	0.0235			
White blood cells	0.0061			
Cervix	0.0319			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0136
Gastrointestinal	0.0111	Ovary_n	0.0000
Brain	0.0813	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.4149
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0145	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0154
Kidney	0.0309	Lung	0.0573
Placenta	0.0121	Nerves	0.0040
Prostate	0.0249	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 107

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0102	0.0132	0.7777	1.2858
Ovary	0.0153	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0208	0.0000	undef
Gastrointestinal	0.0119	0.0075	1.5849	0.6309
Brain	0.0307	0.0093	3.3134	0.3018
Hematopoietic	0.0111	0.0144	0.7714	1.2964
Skin	0.0094	0.0379	0.2470	4.0483
Hepatic	0.0441	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0170	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0229	0.0245	0.9314	1.0737
Muscle-skeleton	0.0097	0.0000	undef	0.0000
Kidney	0.0034	0.0120	0.2856	3.5020
Pancreas	0.0190	0.0205	0.9252	1.0808
Penis	0.0083	0.0110	0.7479	1.3371
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0065	0.0106	0.6142	1.6282
Uterus-myometrium	0.0405	0.0000	undef	0.0000
Uterus-general	0.0000	0.0272	0.0000	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0191			
Cervix	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development		Breast
Gastrointestinal	0.0278	Ovary_n
Brain	0.0083	Ovary_t
Hematopoietic	0.0188	Endocrine tissue
Skin	0.0079	Fetal
Hepatic	0.0000	Gastrointestinal
Heart-blood vessels	0.0000	Hematopoietic
Lung	0.0107	Skin-muscle
Suprarenal gland	0.0072	Testicles
Kidney	0.0254	Lung
Placenta	0.0185	Nerves
Prostate	0.0000	Prostate
Sensory organs	0.0000	Sensory Organs
		Uterus_n

Electronic Northern for SEQ. ID NO.: 108

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000 undef	
Breast	0.0051	0.0132	0.3889 2.5715	
Small intestine	0.0061	0.0000	undef 0.0000	
Ovary	0.0000	0.0156	0.0000 undef	
Endocrine tissue	0.0034	0.0125	0.2717 3.6805	
Gastrointestinal	0.0077	0.0000	undef 0.0000	
Brain	0.0037	0.0062	0.6000 1.6668	
Hematopoietic	0.0080	0.0000	undef 0.0000	
Skin	0.0037	0.0000	undef 0.0000	
Hepatic	0.0048	0.0129	0.3676 2.7200	
Heart	0.0032	0.0000	undef 0.0000	
Testicles	0.0058	0.0000	undef 0.0000	
Lung	0.0093	0.0123	0.7621 1.3122	
Stomach-esophagus	0.0097	0.0153	0.6303 1.5866	
Muscle-skeleton	0.0034	0.0000	undef 0.0000	
Kidney	0.0027	0.0068	0.3965 2.5219	
Pancreas	0.0017	0.0055	0.2991 3.3428	
Penis	0.0090	0.0267	0.3369 2.9678	
Prostate	0.0392	0.0213	1.8425 0.5427	
Prostate	0.0000	0.0000	undef undef	
Uterus-endometrium	0.0000	0.0000	undef undef	
Uterus-myometrium	0.0051	0.0000	undef 0.0000	
Uterus-general	0.0032			
Breast hyperplasia	0.0238			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0104			
White blood cells	0.0106			
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0056	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0105
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0285
Lung	0.0000	Skin-muscle	0.0324
Suprarenal gland	0.0072	Testicles	0.0077
Kidney	0.0000	Lung	0.0246
Placenta	0.0247	Nerves	0.0020
Prostate	0.0000	Prostate	0.0410
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

Electronic Northern for SEQ. ID NO.: 110

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0102	0.7627	1.3111
Small intestine	0.0166	0.0282	0.5898	1.6955
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0060	0.0390	0.1535	6.5146
Gastrointestinal	0.0392	0.0527	0.7439	1.3442
Brain	0.0153	0.0370	0.4142	2.4145
Hematopoietic	0.0059	0.0072	0.8228	1.2153
Skin	0.0080	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0000	0.0129	0.0000	undef
Testicles	0.0064	0.0687	0.0925	10.8088
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0239	0.0470	0.5080	1.9684
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0120	0.0120	0.9994	1.0006
Pancreas	0.0299	0.0000	undef	0.0000
Penis	0.0182	0.0110	1.6453	0.6078
Prostate	0.0210	0.0000	undef	0.0000
Uterus-endometrium	0.0305	0.0106	2.8662	0.3489
Uterus-myometrium	0.0203	0.1055	0.1920	5.2070
Uterus-general	0.0076	0.0136	0.5611	1.7821
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0352			
Seminal vesicle	0.0446			
Sensory organs	0.0267			
White blood cells	0.0353			
Cervix	0.0147			
	0.0106			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0068
Brain	0.0222	Ovary_t	0.1595
Hematopoietic	0.0000	Endocrine tissue	0.0101
Skin	0.0197	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0408
Heart-blood vessels	0.0000	Hematopoietic	0.0366
Lung	0.0178	Skin-muscle	0.0000
Suprarenal gland	0.0145	Testicles	0.0259
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0410
Prostate	0.0000	Prostate	0.0151
Sensory organs	0.0000	Sensory Organs	0.0342
	0.0126	Uterus_n	0.0155
			0.0125



	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0460	0.2542	3.9333
Breast	0.0192	0.0376	0.5104	1.9593
Small intestine	0.0000	0.0496	0.0000	undef
Ovary	0.0030	0.0234	0.1279	7.8175
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0062	0.0102	0.6096	1.6403
Stomach-esophagus	0.0193	0.0000	undef	0.0000
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0271	0.0137	1.9826	0.5044
Pancreas	0.0132	0.0221	0.5983	1.6714
Penis	0.0030	0.0267	0.1123	8.9035
Prostate	0.0240	0.0298	0.8043	1.2434
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000	0.0954	0.0000	undef
Breast hyperplasia	0.0352			
Prostate hyperplasia	0.0149			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0106			

FETUS	% frequency	STANDARDIZED/SUBTRACTED LIBRARIES	% frequency
Development		Breast	0.0408
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0608
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0122
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0246
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus n	0.0000

Electronic Northern for SEQ. ID NO.: 112

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0039	0.0051	0.7627	1.3111
Small intestine	0.0051	0.0207	0.2475	4.0410
Ovary	0.0123	0.0000	undef	0.0000
Endocrine tissue	0.0030	0.0338	0.0886	11.2920
Gastrointestinal	0.0017	0.0025	0.6792	1.4722
Brain	0.0038	0.0185	0.2071	4.8289
Hematopoietic	0.0022	0.0092	0.2400	4.1669
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0037	0.0847	0.0433	23.0839
Heart	0.0000	0.0000	undef	undef
Testicles	0.0053	0.0275	0.1927	5.1882
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0041	1.0161	0.9842
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0109	0.0000	undef	0.0000
Penis	0.0033	0.0055	0.5983	1.6714
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0044	0.0000	undef	0.0000
Uterus-myometrium	0.0135	0.0000	undef	0.0000
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0051	0.0000	undef	0.0000
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0030			
Sensory organs	0.0178			
White blood cells	0.0118			
Cervix	0.0009			
	0.0213			

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast
Gastrointestinal	Ovary_n
Brain	Ovary_t
Hematopoietic	Endocrine tissue
Skin	Fetal
Hepatic	Gastrointestinal
Heart-blood vessels	Hematopoietic
Lung	Skin-muscle
Suprarenal gland	Testicles
Kidney	Lung
Placenta	Nerves
Prostate	Prostate
Sensory organs	Sensory Organs
	Uterus_n

Electronic Northern for SEQ. ID NO.: 113

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0409	0.2860	3.4963
Breast	0.0256	0.0376	0.6805	1.4694
Small intestine	0.0399	0.0000	undef	0.0000
Ovary	0.0090	0.0390	0.2303	4.3431
Endocrine tissue	0.0477	0.0702	0.6792	1.4722
Gastrointestinal	0.0479	0.0231	2.0708	0.4829
Brain	0.0229	0.0349	0.6564	1.5234
Hematopoietic	0.0281	0.0000	undef	0.0000
Skin	0.0624	0.0000	undef	0.0000
Hepatic	0.0048	0.0259	0.1838	5.4400
Heart	0.0519	0.0000	undef	0.0000
Testicles	0.0230	0.0468	0.4920	2.0326
Lung	0.0270	0.0491	0.5504	1.8170
Stomach-esophagus	0.0387	0.0230	1.6807	0.5950
Muscle-skeleton	0.0377	0.0840	0.4487	2.2286
Kidney	0.0462	0.0411	1.1235	0.8901
Pancreas	0.0116	0.0276	0.4188	2.3877
Penis	0.0150	0.0533	0.2808	3.5614
Prostate	0.0283	0.0490	0.5786	1.7284
Uterus-endometrium	0.0541	0.0528	1.0243	0.9763
Uterus-myometrium	0.0305	0.0272	1.1223	0.8911
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0267			
Sensory organs	0.0353			
White blood cells	0.0312			
Cervix	0.0213			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0139	Breast	0.0000
Gastrointestinal	0.0611	Ovary_n	0.1595
Brain	0.0063	Ovary_t	0.0000
Hematopoietic	0.0157	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0029
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0320	Hematopoietic	0.0000
Lung	0.0397	Skin-muscle	0.0000
Suprarenal gland	0.0507	Testicles	0.0164
Kidney	0.0247	Lung	0.0050
Placenta	0.0303	Nerves	0.0068
Prostate	0.1247	Prostate	0.0000
Sensory organs	0.0377	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 115

	NORMAL % frequency	TUMOR % frequency	Ratios N/T      T/N	
Bladder	0.0039	0.0051	0.7627	1.3111
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0702	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0192	0.0185	1.0354	0.9658
Brain	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0052	0.0020	2.5402	0.3937
Lung	0.0193	0.0230	0.8404	1.1900
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0110	0.1496	6.6857
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0954	0.0000	undef
Uterus-myometrium	0.0000			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0118			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

FETUS % frequency		STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0000	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0010
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0167
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 116

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0038	0.0038	1.0208	0.9796
Small intestine	0.0061	0.0165	0.3707	2.6973
Ovary	0.0030	0.0208	0.1439	6.9489
Endocrine tissue	0.0102	0.0025	4.0755	0.2454
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0030	0.0031	0.9599	1.0417
Hematopoietic	0.0094	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0058	0.0000	undef	0.0000
Testicles	0.0073	0.0123	0.5927	1.6872
Lung	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0051	0.0000	undef	0.0000
Muscle-skeleton	0.0081	0.0068	1.1896	0.8406
Kidney	0.0017	0.0055	0.2991	3.3428
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0065	0.0021	3.0709	0.3256
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0064			
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0078			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0032
Lung	0.0036	Skin-muscle	0.0154
Suprarenal gland	0.0254	Testicles	0.0082
Kidney	0.0124	Lung	0.0060
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0208
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 117

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0128	0.6102	1.6389
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0208	0.0000	undef
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0517	0.0879	0.5886	1.6991
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0381	0.0518	0.7353	1.3600
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0164	0.0635	15.7470
Lung	0.0290	0.0230	1.2605	0.7933
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0033	0.0110	0.2991	3.3428
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0022	0.0043	0.5118	1.9538
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0051	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs				
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0051
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0000
Sensory organs		Sensory Organs	0.0000
		Uterus_n	0.0000

Electronic Northern for SEQ. ID NO.: 120

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0013	0.0056	0.2268	4.4083
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0022	0.0031	0.7200	1.3890
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0042	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0027	0.0068	0.3965	2.5219
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0000	0.0000	undef
Uterus-general	0.0032	0.0000	undef	0.0000
Breast hyperplasia	0.0030	0.0000	undef	0.0000
Prostate hyperplasia	0.0000	0.0000	undef	undef
Seminal vesicle	0.0043	0.0068	0.0000	undef
Sensory organs	0.0000	0.0000	undef	0.0000
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0023
Hepatic	0.0260	Gastrointestinal	0.0000
Heart-blood vessels	0.0036	Hematopoietic	0.0114
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0082
Kidney	0.0062	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0249	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 121

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0153	0.7627	1.3111
Breast	0.0026	0.0132	0.1944	5.1431
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0000	0.0156	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0019	0.0046	0.4142	2.4145
Brain	0.0030	0.0062	0.4800	2.0835
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.1760	0.0518	3.4008	0.2941
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0058	0.0117	0.4920	2.0326
Lung	0.0010	0.0082	0.1270	7.8735
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0188	0.0060	3.1411	0.3184
Kidney	0.0081	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Penis	0.0000	0.0000	undef	undef
Prostate	0.0174	0.0277	0.6299	1.5875
Uterus-endometrium	0.0000	0.0528	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0954		0.0000	undef
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0119			
Seminal vesicle	0.0000			
Sensory organs	0.0235			
White blood cells	0.0009			
Cervix	0.0000			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0203
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0035
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0071	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000



Electronic Northern for SEQ. ID NO.: 122

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1053	0.1125	0.9361	1.0683
Breast	0.1164	0.1015	1.1468	0.8720
Small intestine	0.0491	0.0662	0.7415	1.3487
Ovary	0.0479	0.1015	0.4723	2.1173
Endocrine tissue	0.0562	0.0251	2.2415	0.4461
Gastrointestinal	0.1015	0.1758	0.5777	1.7311
Brain	0.0296	0.1273	0.2322	4.3058
Hematopoietic	0.0535	0.0000	undef	0.0000
Skin	0.2166	0.0000	undef	0.0000
Hepatic	0.0809	0.1035	0.7813	1.2800
Heart	0.4133	0.2612	1.5825	0.6319
Testicles	0.0748	0.0468	1.5989	0.6254
Lung	0.1506	0.1227	1.2278	0.8145
Stomach-esophagus	0.2126	0.1073	1.9808	0.5048
Muscle-skeleton	0.0805	0.1680	0.4793	2.0863
Kidney	0.0543	0.0890	0.6100	1.6393
Pancreas	0.0562	0.1712	0.3281	3.0479
Penis	0.1497	0.2399	0.6240	1.6026
Prostate	0.0850	0.0362	2.3483	0.4258
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0457	0.1019	0.4489	2.2276
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0991			
Prostate hyperplasia	0.0832			
Seminal vesicle	0.0801			
Sensory organs	0.1059			
White blood cells	0.0720			
Cervix	0.0639			

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0835	Breast	0.0544
Gastrointestinal	0.0361	Ovary_n	0.0000
Brain	0.0063	Ovary_t	0.0101
Hematopoietic	0.0433	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0466
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0961	Hematopoietic	0.0000
Lung	0.0867	Skin-muscle	0.0421
Suprarenal gland	0.0761	Testicles	0.0000
Kidney	0.0309	Lung	0.1474
Placenta	0.1151	Nerves	0.0110
Prostate	0.5984	Prostate	0.0205
Sensory organs	0.0251	Sensory Organs	0.0000
		Uterus_n	0.0042

Electronic Northern for SEQ. ID NO.: 123

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0026	1.5254	0.6555
Breast	0.0013	0.0019	0.6805	1.4694
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0000	0.0182	0.0000	undef
Endocrine tissue	0.0017	0.0075	0.2264	4.4166
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0030	0.0021	1.4399	0.6945
Hematopoietic	0.0013	0.0000	undef	0.0000
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0053	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0010	0.0061	0.1693	5.9051
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0086	0.0060	1.4278	0.7004
Kidney	0.0027	0.0205	0.1322	7.5658
Pancreas	0.0066	0.0055	1.1966	0.8357
Penis	0.0060	0.0000	undef	0.0000
Prostate	0.0044	0.0021	2.0473	0.4885
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0076	0.0068	1.1223	0.8911
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0064			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells				
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development	0.0000	Breast	0.0000
Gastrointestinal	0.0028	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0134
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0130
Suprarenal gland	0.0254	Testicles	0.0000
Kidney	0.0062	Lung	0.0164
Placenta	0.0182	Nerves	0.0030
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

## Electronic Northern for Seq. ID: 258

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0000	0.0047	0.0000 undef
Large intestine	0.0018	0.0014	1.2524 0.7985
Small intestine	0.0019	0.0000	undef 0.0000
Ovary	0.0027	0.0213	0.1288 7.7625
Endocrine tissue	0.0000	0.0167	0.0000 undef
Brain	0.0064	0.0000	undef 0.0000
Skin	0.0012	0.0010	1.1605 0.8617
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0051	0.0000	undef 0.0000
Lung	0.0080	0.0118	0.6786 1.4737
Stomach-esophagus	0.0029	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidney	0.0000	0.0037	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0017	0.0000	undef 0.0000
T lymphoma	0.0019	0.0000	undef 0.0000
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0040		
Penis	0.0000		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0030
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0121
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 259

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder				
Breast	0.0000	0.0000	undef	undef
Large intestine	0.0117	0.0023	4.9785	0.2009
Small intestine	0.0070	0.0014	5.0097	0.1996
Ovary	0.0000	0.0057	0.0000	undef
Endocrine tissue	0.0082	0.0000	undef	0.0000
Brain	0.0000	0.0119	0.0000	undef
Skin	0.0032	0.0089	0.3621	2.7613
Hepatic	0.0006	0.0000	undef	0.0000
Heart	0.0037	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0081	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0019	0.0000	undef	0.0000
Kidney	0.0145	0.0000	undef	0.0000
Pancreas	0.0000	0.0037	0.0000	undef
Prostate	0.0022	0.0000	undef	0.0000
T lymphoma	0.0017	0.0000	undef	0.0000
Uterus	0.0019	0.0000	undef	0.0000
White blood cells	0.0025	0.0075	0.3381	2.9576
Hematopoietic	0.0059	0.0138	0.4284	2.3344
Penis	0.0000	0.0000	undef	undef
Seminal vesicle	0.0027			
Sensory organs	0.0080			
	0.0141			
	0.0000			

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary Uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 260

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0023	0.0000	undef
Large intestine	0.0062	0.0000	undef	0.0000
Small intestine	0.0019	0.0085	0.2243	4.4591
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0525	0.0000	undef
Brain	0.0032	0.0071	0.4527	2.2091
Skin	0.0023	0.0020	1.1605	0.8617
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0063	0.0000	undef
Testicles	0.0051	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0088	0.0037	2.3680	0.4223
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0017	0.0000	undef	0.0000
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0083	0.0000	undef	0.0000
T lymphoma	0.0028	0.0013	2.1706	0.4607
Uterus	0.0051	0.0224	0.2254	4.4364
White blood cells	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0027	0.0304	0.0902	11.0896
Penis	0.0013			
Seminal vesicle	0.0000			
Sensory organs	0.0070			
	0.0000			

FETUS  
% freq.

Development	
Gastrointestinal	0.0139
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0107
Adrenal gland	0.0036
Kidney	0.0000
Placenta	0.0062
Prostate	0.0000
Sensory organs	0.0000
	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0098
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0060
Nerves	0.0000
Kidney t	0.0000
Ovary Uterus	0.0113
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seg. ID: 261

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma				
Bladder	0.0025	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Large intestine	0.0009	0.0014	0.6262	1.5969
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0027	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0191	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Skin	0.0006	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0019	0.0055	0.0000	undef
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0015	0.0000	undef	0.0000
White blood cells	0.0034	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0000			
Seminal vesicle	0.0070			
Sensory organs	0.0000			

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0023
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0023
Ovary uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 262

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0150	0.0000	undef 0.0000
Breast	0.0156	0.0023	6.6380 0.1506
Large intestine	0.0158	0.0056	2.8179 0.3549
Small intestine	0.0038	0.0028	1.3456 0.7432
Ovary	0.0110	0.0320	0.3435 2.9109
Endocrine tissue	0.0178	0.0334	0.5333 1.8752
Brain	0.0064	0.0213	0.3018 3.3136
Skin	0.0081	0.0060	1.3539 0.7386
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0139	0.0190	0.7324 1.3653
Testicles	0.0193	0.0000	undef 0.0000
Lung	0.0080	0.0118	0.6786 1.4737
Stomach-esophagus	0.0175	0.0129	1.3531 0.7390
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0017	0.0111	0.1546 6.4671
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0132	0.0000	undef 0.0000
T lymphoma	0.0104	0.0091	1.1370 0.8795
Uterus	0.0101	0.0149	0.6762 1.4788
White blood cells	0.0192	0.0230	0.8353 1.1971
Hematopoietic	0.0055	0.0304	0.1803 5.5448
Penis	0.0067		
Seminal vesicle	0.0080		
Sensory organs	0.0070		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0000
Hematopoietic	0.0275
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0162
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0454
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0100
Nerves	0.0000
Kidney t	0.0293
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

## Electronic Northern for Seq. ID: 263

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0136	0.9198 1.0872
Breast	0.0039	0.0188	0.2075 4.8204
Large intestine	0.0114	0.0281	0.4070 2.4568
Small intestine	0.0211	0.0142	1.4801 0.6756
Ovary	0.0082	0.0000	undef 0.0000
Endocrine tissue	0.0089	0.0286	0.3111 3.2147
Brain	0.0161	0.0151	1.0599 0.9435
Skin	0.0211	0.0110	1.9234 0.5199
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0046	0.0127	0.3662 2.7307
Testicles	0.0162	0.0000	undef 0.0000
Lung	0.0080	0.0178	0.4523 2.2108
Stomach-esophagus	0.0136	0.0111	1.2278 0.8145
Muscle-skeleton	0.0072	0.0128	0.5666 1.7648
Kidney	0.0188	0.0185	1.0206 0.9799
Pancreas	0.0157	0.0145	1.0831 0.9232
Prostate	0.0083	0.0221	0.3739 2.6743
T lymphoma	0.0123	0.0039	3.1352 0.3190
Uterus	0.0000	0.0149	0.0000 undef
White blood cells	0.0077	0.0230	0.3368 2.9694
Hematopoietic	0.0082	0.0000	undef 0.0000
Penis	0.0094		
Seminal vesicle	0.0107		
Sensory organs	0.0070		
	0.0235		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0107
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0203
Endocrine tissue	0.0000
Fetal	0.0069
Gastrointestinal	0.0488
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0167
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0060
Kidney t	0.0000
Ovary Uterus	0.0158
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000



Electronic Northern for Seq. ID: 264

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0150	0.0136	1.1037 0.9060
Large intestine	0.0273	0.0211	1.2907 0.7748
Small intestine	0.0229	0.0632	0.3618 2.7639
Ovary	0.0268	0.0256	1.0466 0.9555
Endocrine tissue	0.0192	0.0000	undef 0.0000
Brain	0.0089	0.0501	0.1778 5.6255
Skin	0.0193	0.0142	1.3580 0.7364
Hepatic	0.0041	0.0160	0.2539 3.9391
Heart	0.0073	0.0000	undef 0.0000
Testicles	0.0465	0.0254	1.8311 0.5461
Lung	0.0091	0.0412	0.2215 4.5144
Stomach-esophagus	0.0120	0.0000	undef 0.0000
Muscle-skeleton	0.0204	0.0185	1.1050 0.9049
Kidney	0.0290	0.0384	0.7557 1.3233
Pancreas	0.0069	0.0185	0.3711 2.6946
Prostate	0.0537	0.0289	1.8570 0.5385
T lymphoma	0.0380	0.0110	3.4403 0.2907
Uterus	0.0330	0.0130	2.5323 0.3949
White blood cells	0.0051	0.0075	0.6762 1.4788
Hematopoietic	0.0148	0.0138	1.0709 0.9338
Penis	0.0075	0.0000	undef 0.0000
Seminal vesicle	0.0147		
Sensory organs	0.0054		
	0.0000		
	0.0235		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0040
Nerves	0.0000
Kidney t	0.0090
Ovary uterus	0.0121
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 265

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder			
Breast	0.0000	0.0272	0.0000 undef
Large intestine	0.0117	0.0023	4.9785 0.2009
Small intestine	0.0141	0.0155	0.9109 1.0979
Ovary	0.0920	0.0968	0.9498 1.0528
Endocrine tissue	0.0247	0.0000	undef 0.0000
Brain	0.0208	0.0882	0.2354 4.2478
Skin	0.0016	0.0000	undef 0.0000
Hepatic	0.0000	0.0010	0.0000 undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0444	0.0000 undef
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0165	0.0111	1.4909 0.6707
Muscle-skeleton	0.0362	0.0128	2.8338 0.3529
Kidney	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0000	0.0166	0.0000 undef
T lymphoma	0.0207	0.0352	0.5895 1.6963
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0030	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0027		
Seminal vesicle	0.0000		
Sensory organs	0.0915		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0278
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0253
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0084
Testicles_n	0.0000
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0113
Ovary Uterus	0.0182
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 266

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0114	0.0000	undef	0.0000
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0055	0.0000	undef	0.0000
Ovary	0.0059	0.0525	0.1131	8.8401
Endocrine tissue	0.0161	0.0035	4.5268	0.2209
Brain	0.0017	0.0000	undef	0.0000
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0071	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0049	0.0037	1.3155	0.7601
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidney	0.0470	0.0048	9.7491	0.1026
Pancreas	0.0033	0.0000	undef	0.0000
Prostate	0.0019	0.0000	undef	0.0000
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0007	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0080			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0020
Nerves	0.0000
Kidney t	0.0023
Ovary uterus	0.0000
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 267

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0000	0.0070	0.0000 undef
Breast	0.0026	0.0014	1.8786 0.5323
Large intestine	0.0000	0.0000	undef undef
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0119	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0029	0.0010	2.9013 0.3447
Skin	0.0000	0.0394	0.0000 undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0030	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0049	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef 0.0000
Muscle-skeleton	0.0034	0.0000	undef undef
Kidney	0.0000	0.0000	undef 0.0000
Pancreas	0.0000	0.0048	0.0000 undef
Prostate	0.0028	0.0000	undef undef
T lymphoma	0.0000	0.0000	undef 0.0000
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0007	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef 0.0000
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0035
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

	Electronic Northern for Seq. ID: 268		RATIOS	
	NORMAL % freq.	TUMOR % freq.	N/T	T/N
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0117	0.0094	1.2446	0.8035
Breast	0.0088	0.0253	0.3479	2.8744
Large intestine	0.0192	0.0028	6.7278	0.1486
Small intestine	0.0192	0.0213	0.9018	1.1089
Ovary	0.0030	0.0143	0.2074	4.8219
Endocrine tissue	0.0193	0.0035	5.4321	0.1841
Brain	0.0081	0.0249	0.3249	3.0774
Skin	0.0184	0.0000	undef	0.0000
Hepatic	0.0093	0.0063	1.4649	0.6826
Heart	0.0112	0.0000	undef	0.0000
Testicles	0.0040	0.0118	0.3393	2.9475
Lung	0.0126	0.0037	3.4204	0.2924
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.0037	3.2472	0.3080
Kidney	0.0157	0.0048	3.2497	0.3077
Pancreas	0.0050	0.0110	0.4487	2.2285
Prostate	0.0104	0.0052	1.9897	0.5026
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0163	0.0092	1.7670	0.5659
White blood cells	0.0110	0.0000	undef	0.0000
Hematopoietic	0.0027			
Penis	0.0054			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

Breast  
Breast\_t  
Large Intestine\_t  
Ovary\_n  
Ovary\_t  
Endocrine tissue  
Fetal  
Gastrointestinal  
Hematopoietic  
Skin-muscle  
Testicles\_n  
Testicles\_t  
Lungs\_n  
Lungs\_t  
Nerves  
Kidney\_t  
Ovary uterus  
Prostate\_n  
Sensory organs  
white blood cells

Electronic Northern for Seq. ID: 269

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0156	0.0047	3.3190 0.3013
Large intestine	0.0079	0.0014	5.6359 0.1774
Small intestine	0.0096	0.0057	1.6820 0.5945
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0030	0.0191	0.1555 6.4291
Brain	0.0064	0.0018	3.6214 0.2761
Skin	0.0058	0.0060	0.9671 1.0340
Hepatic	0.0037	0.0000	undef 0.0000
Heart	0.0000	0.0127	0.0000 undef
Testicles	0.0091	0.0000	undef 0.0000
Lung	0.0080	0.0000	undef 0.0000
Stomach-esophagus	0.0068	0.0037	1.8417 0.5430
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0034	0.0111	0.3093 3.2335
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0083	0.0110	0.7479 1.3371
T lymphoma	0.0057	0.0117	0.4823 2.0732
Uterus	0.0025	0.0000	undef 0.0000
White blood cells	0.0044	0.0092	0.4819 2.0750
Hematopoietic	0.0034	0.0000	undef 0.0000
Penis	0.0027		
Seminal vesicle	0.0188		
Sensory organs	0.0141		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0107
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0068
Prostate_n	0.0000
Sensory organs	0.0077
White blood cells	0.0000

Electronic Northern for Seq. ID: 270

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0075	0.0000	undef 0.0000
Breast	0.0156	0.0047	3.3190 0.3013
Large intestine	0.0167	0.0197	0.8499 1.1767
Small intestine	0.0307	0.0199	1.5378 0.6503
Ovary	0.0082	0.0213	0.3865 2.5875
Endocrine tissue	0.0059	0.0334	0.1778 5.6255
Brain	0.0321	0.0248	1.2934 0.7732
Skin	0.0365	0.0170	2.1504 0.4650
Hepatic	0.0257	0.0000	undef 0.0000
Heart	0.0000	0.0127	0.0000 undef
Testicles	0.0426	0.0000	undef 0.0000
Lung	0.0161	0.0118	1.3571 0.7369
Stomach-esophagus	0.0272	0.0222	1.2278 0.8144
Muscle-skeleton	0.0072	0.0000	undef 0.0000
Kidney	0.0137	0.0074	1.8555 0.5389
Pancreas	0.0246	0.0145	1.7022 0.5875
Prostate	0.0050	0.0000	undef 0.0000
T lymphoma	0.0179	0.0065	2.7494 0.3637
Uterus	0.0177	0.0672	0.2630 3.8026
White blood cells	0.0118	0.0046	2.5703 0.3891
Hematopoietic	0.0219	0.0000	undef 0.0000
Penis	0.0147		
Seminal vesicle	0.0188		
Sensory organs	0.0281		
	0.0000		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0167
Brain	0.0188
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0356
Lung	0.0108
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.1595
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0110
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0281
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0061
Sensory organs	0.0232
White blood cells	0.0000

Electronic Northern for Seq. ID: 271

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0125	0.0407	0.3066 3.2617
Breast	0.0117	0.0164	0.7112 1.4061
Large intestine	0.0123	0.0098	1.2524 0.7985
Small intestine	0.0057	0.0057	1.0092 0.9909
Ovary	0.0165	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0143	0.2074 4.8219
Brain	0.0096	0.0195	0.4938 2.0250
Skin	0.0122	0.0070	1.7408 0.5745
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0093	0.0000	undef 0.0000
Testicles	0.0071	0.0137	0.5169 1.9347
Lung	0.0201	0.0059	3.3928 0.2947
Stomach-esophagus	0.0117	0.0148	0.7893 1.2669
Muscle-skeleton	0.0072	0.0320	0.2267 4.4110
Kidney	0.0086	0.0000	undef 0.0000
Pancreas	0.0045	0.0096	0.4642 2.1540
Prostate	0.0017	0.0055	0.2992 3.3427
T lymphoma	0.0066	0.0117	0.5627 1.7770
Uterus	0.0126	0.0149	0.8453 1.1830
White blood cells	0.0059	0.0322	0.1836 5.4469
Hematopoietic	0.0062	0.0304	0.2029 4.9287
Penis	0.0107		
Seminal vesicle	0.0000		
Sensory organs	0.0141		
	0.0235		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0250
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0152
Endocrine tissue	0.0000
Fetal	0.0220
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0421
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0211
Nerves	0.0000
Kidney t	0.0248
Ovary Uterus	0.0000
Prostate n	0.0232
Sensory organs	0.0000
White blood cells	



## Electronic Northern for Seq. ID: 272

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0136	0.1840 5.4361
Breast	0.0039	0.0117	0.3319 3.0130
Large intestine	0.0246	0.0070	3.5068 0.2852
Small intestine	0.0287	0.0399	0.7208 1.3873
Ovary	0.0082	0.0426	0.1932 5.1750
Endocrine tissue	0.0148	0.0381	0.3889 2.5717
Brain	0.0161	0.0266	0.6036 1.6568
Skin	0.0220	0.0130	1.6961 0.5896
Hepatic	0.0110	0.0000	undef 0.0000
Heart	0.0000	0.0381	0.0000 undef
Testicles	0.0132	0.0000	undef 0.0000
Lung	0.0040	0.0000	undef 0.0000
Stomach-esophagus	0.0214	0.0129	1.6538 0.6047
Muscle-skeleton	0.0000	0.0064	0.0000 undef
Kidney	0.0069	0.0000	undef 0.0000
Pancreas	0.0134	0.0193	0.6964 1.4360
Prostate	0.0264	0.0276	0.9573 1.0446
T lymphoma	0.0075	0.0104	0.7235 1.3821
Uterus	0.0227	0.0373	0.6086 1.6431
White blood cells	0.0059	0.0138	0.4284 2.3344
Hematopoietic	0.0082	0.0607	0.1353 7.3931
Penis	0.0053		
Seminal vesicle	0.0161		
Sensory organs	0.0141		
	0.0000		

FETUS  
% freq.

Development	0.0278
Gastrointestinal	0.0056
Brain	0.0375
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0142
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0061
Prostate	0.0499
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0136
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0195
Lungs_n	0.0000
Lungs_t	0.0121
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0061
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	

Electronic Northern for Seq. ID: 273

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0025	0.0000	undef 0.0000
Breast	0.0078	0.0188	0.4149 2.4104
Large intestine	0.0079	0.0112	0.7045 1.4195
Small intestine	0.0019	0.0057	0.3364 2.9727
Ovary	0.0055	0.0000	undef 0.0000
Endocrine tissue	0.0030	0.0215	0.1383 7.2328
Brain	0.0080	0.0053	1.5089 0.6627
Skin	0.0041	0.0070	0.5803 1.7234
Hepatic	0.0147	0.0000	undef 0.0000
Heart	0.0046	0.0000	undef 0.0000
Testicles	0.0203	0.0000	undef 0.0000
Lung	0.0000	0.0355	0.0000 undef
Stomach-esophagus	0.0039	0.0111	0.3508 2.8506
Muscle-skeleton	0.0145	0.0128	1.1335 0.8822
Kidney	0.0120	0.0074	1.6236 0.6159
Pancreas	0.0000	0.0048	0.0000 undef
Prostate	0.0000	0.0276	0.0000 undef
T lymphoma	0.0085	0.0065	1.3023 0.7679
Uterus	0.0303	0.0149	2.0287 0.4929
White blood cells	0.0133	0.0092	1.4458 0.6917
Hematopoietic	0.0205	0.0000	undef 0.0000
Penis	0.0027		
Seminal vesicle	0.0054		
Sensory organs	0.0000		
	0.0118		

FETUS  
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0118
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0213
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0124
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0152
Fetal	0.0245
Gastrointestinal	0.0023
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0098
Nerves	0.0000
Kidney t	0.0060
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0000
White blood cells	0.0000

## 2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S. If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S. Its electronic Northern Blot will

accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  ( $i$ : iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from ovarian tumor tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

**Example 4****Mapping of nucleic acid sequences on the human genome**

Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

### **Example 5**

#### **Obtaining genomic DNA sequences (BAC clones)**

The genomic BAC clones that contain the corresponding cDNAs (<http://www.tree.caltech.edu/>; Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797) were isolated with the procedure of "down-to-the-well." In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is moved into a certain raster, so that the DNA of these clones with a specific PCR can be studied. In doing so, "pooling" of the DNA of different BAC clones takes place. Combinatorial analysis makes it possible to determine the clones that contain the desired DNA. By fixing the clones, the address of the clones in the library can be determined. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries used were CITB B and CITB C:

Seq. ID No.

Identified BACs

4	195/N/3	206/P/3	384/I/3	323/G/9	
5	222/B/10	404/E/10	526/F/20	565/P/11	279/F/14
9	501/L/21				
11	490/P/4	321/I/23	410/F/5	443/N/20	
19	311/A/19	505/F/17	216/D/8	219/C/22	
29	382/N/10	539/L/7			
31	530/D/11				
35	503/N/10				
37	547/D/16	215/P/16	439/K/6		
39	216/L/9	512/F/5	203/J/15		
45	205/K/7	250/H/22	283/C/17	528/B/20	402/L/11
80	371/A/20	470/L/3	495/L/3		
92	254/M/9	376/O/12	421/L/18	429/J/19	
112	243/O/14	520/K/15	565/J/17	565/J/24	

**TABLE I**

Col. 1 - Seq. ID No.  
Col. 2 - Expression  
Col. 3 - Function  
Col. 4 - Modules  
Col. 5 - Cytogenetic localization  
Col. 6 - Nearest marker



TABLE I

Seq. ID No.	Expression	Function
1	Overexpressed in ovarian tumor tissue	Unknown
2	Overexpressed in ovarian tumor tissue	Unknown
3	Overexpressed in ovarian tumor tissue	Unknown
4	Overexpressed in ovarian tumor tissue	P52r1PK
5	Overexpressed in ovarian tumor tissue	Unknown
6	Overexpressed in ovarian tumor tissue	Unknown
7	Overexpressed in ovarian tumor tissue	Unknown
8	Overexpressed in ovarian tumor tissue	Unknown
9	Overexpressed in ovarian tumor tissue	Unknown
10	Overexpressed in ovarian tumor tissue	Unknown
12	Overexpressed in ovarian tumor tissue	Unknown
13	Overexpressed in ovarian tumor tissue	Unknown
15	Overexpressed in ovarian tumor tissue	Unknown
16	Overexpressed in ovarian tumor tissue	Unknown
18	Overexpressed in ovarian tumor tissue	Unknown
19	Overexpressed in ovarian tumor tissue	Unknown

**TABELLE I**

Seq ID No.	Expression	Funktion	Module	Cytogetnelische Lokallisation	nearest marker
1	in Ovarlurnorgewebe überexprimiert	unbekannt		1p31.1-p34.1	SHGC-2542,2540,2456; D1S448- D1S500;; WI-6555; D1S198-D1S462
2	in Ovarlurnorgewebe überexprimiert	unbekannt		2p22.3-p23.3	SGC32173; D2S174-D2S390;; TIGR- A006H24; D2S392-D2S390
3	in Ovarlurnorgewebe überexprimiert	unbekannt		4p15.1	WI-15951 (D4S1043-SHGC-16179)
4	in Ovarlurnorgewebe überexprimiert	P52IPK		11q13.5 - q14.1	SHGC-31396 (SHGC-32287, D11S4681)
5	in Ovarlurnorgewebe überexprimiert	unbekannt		1q22	SHGC-31641
6	in Ovarlurnorgewebe überexprimiert	unbekannt		13q33.1 - q34	AFM310yds
7	in Ovarlurnorgewebe überexprimiert	unbekannt		8q11.23-q12.1	SHGC-32002; D8S1828-D8S507
8	in Ovarlurnorgewebe überexprimiert	unbekannt		4q24	SHGC-36699
9	in Ovarlurnorgewebe überexprimiert	unbekannt	PRO_RICH	2q35	SHGH-32531 (D2S1297, SHGC-35278)
10	in Ovarlurnorgewebe überexprimiert	unbekannt	PHD		
12	in Ovarlurnorgewebe überexprimiert	unbekannt		5q23.3-q31.1	AFM200ya9=D5S414
13	in Ovarlurnorgewebe überexprimiert	unbekannt		3p23	WI-6841; D3S1599-D3S1583
15	in Ovarlurnorgewebe überexprimiert	unbekannt		6q22.1-q24.3	SHGC-33316; D6S453-D6S311
16	in Ovarlurnorgewebe überexprimiert	unbekannt	NLS_BP	10p15.3	CDa11h03; D10S533-D10S594., SHGC- 11812; D10S558-D10S591
18	in Ovarlurnorgewebe überexprimiert	unbekannt	Ribosomal_L24e	15q21.3-q22.1	Cda17g12; D15S209-D15S198
19	in Ovarlurnorgewebe überexprimiert	unbekannt		11q14.3	SHGC-36010 (D11S1979, D11S1887)

Seq. ID No.	Expression	Function
20	Overexpressed in ovarian tumor tissue	Unknown
21	Overexpressed in ovarian tumor tissue	Unknown
22	Overexpressed in ovarian tumor tissue	Unknown
23	Overexpressed in ovarian tumor tissue	Unknown
24	Overexpressed in ovarian tumor tissue	Unknown
25	Overexpressed in ovarian tumor tissue	Branchio-oto-renal syndrome candidate gene
26	Overexpressed in ovarian tumor tissue	Unknown
27	Overexpressed in ovarian tumor tissue	Unknown
28	Overexpressed in ovarian tumor tissue	Unknown
29	Overexpressed in ovarian tumor tissue	Unknown
30	Overexpressed in ovarian tumor tissue	Unknown
31	Overexpressed in ovarian tumor tissue	Unknown
32	Overexpressed in ovarian tumor tissue	Partially homologous to R. norvegicus calpain
33	Overexpressed in ovarian tumor tissue	Partially homologous to human mRNA for fungal sterol-C5-desaturase homolog
34	Overexpressed in ovarian tumor tissue	Partially homologous to human GPx-3 mRNA for plasma glutathione peroxidase
35	Overexpressed in ovarian tumor tissue	Partially homologous to homo sapiens CHD2 mRNA

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
20	in Ovariumorgewebe überexprimiert	unbekannt		3q22.2-3q22.3	SHGC-34629 (SHGC-30855, SGC32794)
21	in Ovariumorgewebe überexprimiert	unbekannt		3q26.33-q29	AFM308yl1 (D3S2363, D3S3669)
22	in Ovariumorgewebe überexprimiert	unbekannt		7q11.23	SHGC-37054
23	in Ovariumorgewebe überexprimiert	unbekannt			
24	in Ovariumorgewebe überexprimiert	unbekannt		4q28.1-q31.1	WI-30941;SGC30941; D4S1580-D4S427
25	in Ovariumorgewebe überexprimiert	Branchio-olo-renal syndrome candidate gene		7q32.3-q33	AFMc024we9
26	in Ovariumorgewebe überexprimiert	unbekannt	NLS_BP	17q23.3	SHGC-64257
27	in Ovariumorgewebe überexprimiert	unbekannt		17p12-p13.2	SHGC-31370 (SHGC-35547-SHGC-35513)
28	in Ovariumorgewebe überexprimiert	unbekannt		10q22.3	Cda0wf11, TIGR-A001X23;D10S607-D10S201
29	in Ovariumorgewebe überexprimiert	unbekannt		11q13.2-q13.5	WI-14303; D11S4136-D11S1314; TIGR-A005U01; D11S913-D11S1314/RH;SHGC-14407
30	in Ovariumorgewebe überexprimiert	unbekannt		7p21.3	SHGC-14339
31	in Ovariumorgewebe überexprimiert	unbekannt		12p12.3	AFMb320va9
32	in Ovariumorgewebe überexprimiert	Partielles Homolog zu R. norvegicus calpain		1q41	SHGC-3992 (D1S2550-D1S2568)
33	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Human mRNA for fungal sterol-C5-desaturase homolog	Thymosin	11q23.3	WI-19895; D11S924-D11S925
34	in Ovariumorgewebe überexprimiert	Partiell homolog zu Human GPx-3 mRNA for plasma glutathione peroxidase	GSHPx	5q33.1	SHGC-10972
35	in Ovariumorgewebe überexprimiert	Partiell Homolog zu Homo sapiens CHD2 mRNA		19q13.13-q13.2	AFMb018wh1

Seq. ID No.	Expression	Function
36	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus formin binding protein 21
38	Overexpressed in ovarian tumor tissue	Human homolog to Tribolium castaneum zinc finger protein
39	Overexpressed in ovarian tumor tissue	Human homolog to S. cerevisiae chromosome II sequence for ORF YBR1725
40	Overexpressed in ovarian tumor tissue	Human homolog to Rattus norvegicus rsly 1p
41	Overexpressed in ovarian tumor tissue	Human homolog to PEC-60=gastrointestinal peptide, swine
42	Overexpressed in ovarian tumor tissue	Human homolog to Mus musculus mCAF1 protein
43	Overexpressed in ovarian tumor tissue	Human homolog to Mouse mitochondrial genome; unidentified reading frame
44	Overexpressed in ovarian tumor tissue	Human homolog to Mouse kidney androgen-regulated protein (KAP)
45	Overexpressed in ovarian tumor tissue	Human homolog to M. musculus Tera
46	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
47	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid T27F7
48	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid K11H12
49	Overexpressed in ovarian tumor tissue	Human homolog to Caenorhabditis elegans cosmid C43E11

Seq ID No.	Expression	Funktion	Module	Cyto genetische Lokalisation	nearest marker
36	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus formin binding protein 21	WW_rsp5_WWP		
38	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Tribolium castaneum zinc finger protein		2p13.1- p16.1:RH: 2p13.1-p13.3	stSG31094; D2S292-D2S145
39	in Ovariumorgewebe überexprimiert	Humanes Homolog zu S; cerevisiae chromosome II sequence for ORF YBR1725		19q12	AFM205yf10 (D19S1080, D19S590)
40	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Rattus norvegicus rsly1p	Sec1	17	
41	in Ovariumorgewebe überexprimiert	Humanes Homolog zu PEC-60=gastrointestinal peptide, swine	kazal		
42	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mus musculus mCAF1 protein		8p22-p23.3	BDA16f11; D8S549-D8S1733 bzw. S280
43	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse mitochondrial genome; Unidentified reading frame	oxidored_q1_N		
44	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Mouse kidney androgen-regulated protein (KAP)		1p36.31-p36.13	SHGC-11461 (D1S2565, SGC32561)
45	in Ovariumorgewebe überexprimiert	Humanes Homolog zu M. musculus Tera		12p11.21- p11.23	SHGC-1349 (D12S1621/D12S1805)
46	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7		19q13.33-qter	SHGC-30173; D19S418-qTEL
47	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid T27F7	PRO_RICH	2p11.1-p11.2	D2S388-D2S2181
48	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid K11H12	UPF0005	10q23.1	SHGC-167+SHGC-11466; D10S551-D10S532
49	in Ovariumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C43E11	PRO_RICH	Xq22.3-Xq25	stSG2963; DXS1059-DXS1047

Seq. ID No.	Expression	Function
50	Overexpressed in ovarian tumor tissue	Human homolog to <i>Caenorhabditis elegans</i> cosmid C40H1
51	Overexpressed in ovarian tumor tissue	Human homolog to <i>C. elegans</i> cosmid K02D10
52	Overexpressed in ovarian tumor tissue	Human homolog to bovine inorganic pyrophosphatase
53	Overexpressed in ovarian tumor tissue	Human homolog to <i>B. laurus</i> mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex
54	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein or others
55	Overexpressed in ovarian tumor tissue	Human homolog to <i>Aplysia californica</i> vesicle-associated membrane protein/synaptobrevin binding protein
56	Overexpressed in ovarian tumor tissue	Human homolog of <i>R. norvegicus</i> intestinal epithelium proliferating cell-associated mRNA sequence
57	Overexpressed in ovarian tumor tissue	Homologous to Bruton's tyrosine kinase
58	Overexpressed in ovarian tumor tissue	dbpB-like protein
59	Overexpressed in ovarian tumor tissue	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein
63	Overexpressed in ovarian tumor tissue	Protease, serine, 2 (trypsin 2)
65	Overexpressed in ovarian tumor tissue	Human annexin IV
67	Overexpressed in ovarian tumor tissue	Human X2 box repressor

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
50	in Ovartumorgewebe überexprimiert	Humanes Homolog zu Caenorhabditis elegans cosmid C40H1		1q22	WI-7155
51	in Ovartumorgewebe überexprimiert	Humanes Homolog zu C. elegans cosmid K02D10		7p11.2-p12.3	Cda1bc08;D7S506-D7S499;; SHGC-17265+11581;D7S499-D7S2429
52	in Ovartumorgewebe überexprimiert	Humanes Homolog zu Bovine inorganic pyrophosphatase	Pyrophosphatase	3q26.1	SHGC-9372
53	in Ovartumorgewebe überexprimiert	Humanes Homolog zu B. taurus mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex		3q13.12-q13.2	D3S1310-D3S1575
54	in Ovartumorgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein aber anders		20q13.33	SHGC-11512
55	in Ovartumorgewebe überexprimiert	Humanes Homolog zu Aplysia californica vesicle-associated membrane protein/synaptobrevin binding protein	PRO_RICH; MSP_DOMAIN	15q25.3-15q26.1	SHGC-69080 (D15S202/D15S1046, D15S1178)
56	in Ovartumorgewebe überexprimiert	Humanes Homolog des R. norvegicus intestinal epithelium proliferating cell-associated mRNA sequence	PRO_RICH	1p32.2-p31.2	SGC34409
57	in Ovartumorgewebe überexprimiert	Homolog zu Bruton's tyrosine kinase	rrm; PRO_RICH	10q21.1-q22.1	WI-11265; D10S581-D10S210
58	in Ovartumorgewebe überexprimiert	dbpB-like protein	CSD; PRO_RICH	15q25.3-15q26.1	AFM282wg5=D15S202 (D15S1046;D15S1187)
59	in Ovartumorgewebe überexprimiert	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	PRO_RICH	2p25.2-p25.1	
63	in Ovartumorgewebe überexprimiert	Protease, serine, 2 (trypsin 2)	trypsin	7q35	SHGC-16894
65	in Ovartumorgewebe überexprimiert	Humanes Annexin IV	annexin	2p13.1-p16.1	SHGC-9858
67	in Ovartumorgewebe überexprimiert	Human X2 box repressor		16q12.1-q22.1	WI-6174; D16S408-D16S3089;;Cda01g10; D16S419-D16S415



Seq. ID No.	Expression	Function
68	Overexpressed in ovarian tumor tissue	Human transcriptional coactivator PC4
69	Overexpressed in ovarian tumor tissue	Human tetratricopeptide repeat protein
70	Overexpressed in ovarian tumor tissue	Human tax1-binding protein TXBP151
72	Overexpressed in ovarian tumor tissue	Human prothymosin alpha
73	Overexpressed in ovarian tumor tissue	Human profilin
74	Overexpressed in ovarian tumor tissue	Human pepsinogen C
76	Overexpressed in ovarian tumor tissue	Human osteopontin
78	Overexpressed in ovarian tumor tissue	Human non-histone chromosomal protein
79	Overexpressed in ovarian tumor tissue	Human mRNA for protein disulfide isomerase-related protein P5
80	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0332
81	Overexpressed in ovarian tumor tissue	Human mRNA for KIAA0078
82	Overexpressed in ovarian tumor tissue	Human mRNA for 90-kDa heat-shock protein
83	Overexpressed in ovarian tumor tissue	Human major nuclear matrix protein
84	Overexpressed in ovarian tumor tissue	Human Ku (p70/p80) subunit
85	Overexpressed in ovarian tumor tissue	Human interferon-induced 17-kDa/15-kDa protein
86	Overexpressed in ovarian tumor tissue	Human hsc70 gene for 71 kd heat shock cognate protein
88	Overexpressed in ovarian tumor tissue	Human gamma-interferon-inducible protein (IP-30)

Seq ID No.	Expression	Funktion	Module	Cytogetische Lokalisation	nearest marker
68	in Ovariumorgewebe überexprimiert	Human transcriptional coactivator PC4		5p15.1	SGC32812; D5S477-D5S651
69	in Ovariumorgewebe überexprimiert	Human tetrapeptide repeat protein		5q33.2-q33.3	TIGR-A002Q13; D5S412-D5S422
70	in Ovariumorgewebe überexprimiert	Human tax1-binding protein TXBP151		7p14.1-p21.3	SGC31789; D7S516-D7S632
72	in Ovariumorgewebe überexprimiert	Human prothymosin alpha			
73	in Ovariumorgewebe überexprimiert	Human profilin	profilin	17p13.3	
74	in Ovariumorgewebe überexprimiert	Human pepsinogen C	asp	6p21.1	SGC35331; D6S426-D6S271
76	in Ovariumorgewebe überexprimiert	Human osteopontin	Osteopontin	4q13.3-q22.1	SHGC-9669; D4S1542-D4S1544
78	in Ovariumorgewebe überexprimiert	Human non-histone chromosomal protein	HMG14_17	21q22.3	
79	in Ovariumorgewebe überexprimiert	Human mRNA for protein disulfide isomerase-related protein P5	thioredoxin	2p23.3-p24.1	SGC31703; D2S287-D2S131;; sISG1958; D2S162-D2S287
80	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0332		3p21.1	SHGC-14798 (D3S4210, SHGC-11985)
81	in Ovariumorgewebe überexprimiert	Human mRNA for KIAA0078	PRO_RICH		SHGC-9647; D7S651-D7S477;; WI-14191; D8S269-D8S1799 +2 weitere auf Chr.8
82	in Ovariumorgewebe überexprimiert	Human mRNA for 90-kDa heat-shock protein	HSP90	4, 11, 1, 6	SHGC-11305
83	in Ovariumorgewebe überexprimiert	Human major nuclear matrix protein	RBD; ZF_MATRIN	5q31.1	SHGC-3183
84	in Ovariumorgewebe überexprimiert	Human Ku (p70/p80) subunit		2q34-q35	SHGC-11966; D2S2382-D2S164;; WI-8140; D2S143-D2S164
85	in Ovariumorgewebe überexprimiert	Human interferon-induced 17-kDa/15-kDa protein	ubiquitin	1p36.31-p36.32	
86	in Ovariumorgewebe überexprimiert	Human hsc70 gene for 71 kd heat shock cognate protein	HSP70	11q23.3-q25	D20S113-D20S97
88	in Ovariumorgewebe überexprimiert	Human gamma-interferon-inducible protein (IP-30)		19p13.13	SHGC-32638; D19S899-D19S407

Seq. ID No.	Expression	Function
89	Overexpressed in ovarian tumor tissue	Human fatty acid binding protein homolog (PA-FABP)
90	Overexpressed in ovarian tumor tissue	Human enhancer of rudimentary homolog
91	Overexpressed in ovarian tumor tissue	Human deleted in split hand/split foot 1 (DSS1)
92	Overexpressed in ovarian tumor tissue	Human decay-accelerating factor mRNA
93	Overexpressed in ovarian tumor tissue	Human chromosome segregation gene homolog CAS
94	Overexpressed in ovarian tumor tissue	Human carcinoma-associated antigen GA733-2, human epithelial glycoprotein (EGP)
95	Overexpressed in ovarian tumor tissue	Human calmodulin
96	Overexpressed in ovarian tumor tissue	Human Bax alpha
97	Overexpressed in ovarian tumor tissue	HUMAN antileukoprotease (ALP)
98	Overexpressed in ovarian tumor tissue	Homo sapiens UDP-galactose-4-epimerase
99	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for putative progesterone binding protein
100	Overexpressed in ovarian tumor tissue	Homo sapiens mRNA for galectin-3
101	Overexpressed in ovarian tumor tissue	Homo sapiens monocyte/macrophage 1g-related receptor MIR-7 (MIR cl-7)
102	Overexpressed in ovarian tumor tissue	Homo sapiens Kunitz-type protease inhibitor
103	Overexpressed in ovarian tumor tissue	Homo sapiens hCPE-R mRNA for CPE-receptor
105	Overexpressed in ovarian tumor tissue	Homo sapiens DNA for amyloid precursor protein
106	Overexpressed in ovarian tumor tissue	Homo sapiens CD24 signal transducer

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
89	in Ovariumorgewebe überexprimiert	Human fatty acid binding protein homologue (PA-FABP)		17p11.2	SHGC-9883
90	in Ovariumorgewebe überexprimiert	Human enhancer of rudimentary homolog	ER	14q22.3-q24.2	WI-8921; D14S63-D14S251
91	in Ovariumorgewebe überexprimiert	Human deleted in split hand/split foot 1 (DSS1)		7q21.3-q22.1	D5S1977-D5S428 (Hs.85215)
92	in Ovariumorgewebe überexprimiert	Human decay-accelerating factor mRNA		1q32.2	SHGC-11228
93	in Ovariumorgewebe überexprimiert	Human chromosome segregation gene homolog CAS	IBN_NT	20q13	
94	in Ovariumorgewebe überexprimiert	Human carcinoma-associated antigen GA733-2, Human epithelial glycoprotein (EGP)	thyroglobulin_1	2p15-p21	AA113218; D2S119-D2S337
95	in Ovariumorgewebe überexprimiert	Human calmodulin	EF_HAND_2	2p16.3-p21	WI-9106; D2S391-D2S123
96	in Ovariumorgewebe überexprimiert	Human Bax alpha	Bcl-2	19q13.3-q13.4	
97	in Ovariumorgewebe überexprimiert	Human antileukoprotease (ALP)	wap	20q13.13-q13.2	WI-6969 (D20S880, SGC34003)
98	in Ovariumorgewebe überexprimiert	Homo sapiens UDP-galactose-4-epimerase	3Beta_HSD	1p36.11	SHGC-11459 (RH420-D1S3295)
99	in Ovariumorgewebe überexprimiert	Homo sapiens mRNA for putative progesterone binding protein		4q31.1	SHGC4-275
100	in Ovariumorgewebe überexprimiert	Homo sapiens mRNA for galectin-3	Gal-bind_lectin	14q12-q22.3	D14S276-D14S66
101	in Ovariumorgewebe überexprimiert	Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7)	7ln_1; G_PROTEIN RECEPTOR 2; PRO_RICH	12q14.2-q14.3	SHGC-33073
102	in Ovariumorgewebe überexprimiert	Homo sapiens Kunitz-type protease inhibitor	Kunitz_BPTi;	19q13.2	TIGR-A007F08; D19S421-D19S408
103	in Ovariumorgewebe überexprimiert	Homo sapiens hCPE-R mRNA for CPE-receptor	PRO_RICH	7q11.23	
105	in Ovariumorgewebe überexprimiert	Homo sapiens DNA for amyloid precursor protein	Kunitz_BPT	21q21.2-q22.11	WI-8962; D21S265-D21S260
106	in Ovariumorgewebe überexprimiert	Homo sapiens CD24 signal transducer		6p21	AFM115xh2, SHGC-13799 - SHGC-32498

Seq. ID No.	Expression	Function
107	Overexpressed in ovarian tumor tissue	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)
108	Overexpressed in ovarian tumor tissue	Histone H2B
110	Overexpressed in ovarian tumor tissue	H. sapiens, gene for membrane cofactor protein
111	Overexpressed in ovarian tumor tissue	H. sapiens TROP-2 gene
112	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Icin protein
113	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for BiP protein
114	Overexpressed in ovarian tumor tissue	H. sapiens HE4 mRNA for extracellular proteinase inhibitor homolog
115	Overexpressed in ovarian tumor tissue	H. sapiens for neutrophil gelatinase associated lipocalin
116	Overexpressed in ovarian tumor tissue	H. sapiens mRNA for Sm protein G
117	Overexpressed in ovarian tumor tissue	H. sapiens for glutathione peroxidase-GI
120	Overexpressed in ovarian tumor tissue	CDC28 protein kinase 2
121	Overexpressed in ovarian tumor tissue	B-factor, properdin
122	Overexpressed in ovarian tumor tissue	Annexin II
123	Overexpressed in ovarian tumor tissue	ADP-ribosylation factor like 1
258	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 2
259	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 3

Seq ID No.	Expression	Funktion	Module	Cytogenetische Lokalisation	nearest marker
107	in Ovariumorgewebe überexprimiert	Homo sapiens Arp2/3 protein complex subunit p16-Arc (ARC16)		1q31.1	SHGC-58249(D1S2602/WI-2775; WI-7265)
108	in Ovariumorgewebe überexprimiert	Histone H2B	histone; Archaeal_histone	6p21.2-p21.31	WI-11733; D6S276-D6S439
110	in Ovariumorgewebe überexprimiert	H.sapiens, gene for Membrane cofactor protein	sushi	1q32.1-q32.2	SHGC-12033; D1S456-D1S2891
111	in Ovariumorgewebe überexprimiert	H.sapiens TROP-2 gene	thyroglobulin_1	1p32.2-p32.3	SHGC-12661; D1S476-D1S220
112	in Ovariumorgewebe überexprimiert	H.sapiens mRNA for Ichn protein		11q14.1	SHGC-31540; D11S4179-D11S937;; SGC31540; D11D911-D11S1352
113	in Ovariumorgewebe überexprimiert	H.sapiens mRNA for BIP protein	HSP70; PRO_RICH	9q33.3-q34.11	WI-6005; D9S282-D9S260
114	in Ovariumorgewebe überexprimiert	H.sapiens HE4 mRNA for extracellular proteinase inhibitor homologue	wap	20q13.2-q13.13	SGC30446; D20S119-D20S197;; WI-30446
115	in Ovariumorgewebe überexprimiert	H.sapiens for neutrophil gelatinase associated lipocalin	lipocalin	9q34	
116	in Ovariumorgewebe überexprimiert	H. sapiens mRNA for Sm protein G		18q21.1	SHGC-8871 (D18S484;D18S851)
117	in Ovariumorgewebe überexprimiert	H. sapiens for glutathione peroxidase-GI	NLS_BP; GSHPx	14q24.1	
120	in Ovariumorgewebe überexprimiert	CDC28 protein kinase 2	CKS	9q21.31-q22.1	SHGC-11955; D9S1812-D9S283;; SGC31294; D9S153-D9S264
121	in Ovariumorgewebe überexprimiert	B-factor, properdin	VWA_DOMAIN; TRYPsin_CATAL; sushi; trypsin		DXS255-DXS426
122	in Ovariumorgewebe überexprimiert	Annexin II	annexin	15q22.1-q22.31	WI-8600+WI-9161; D15S198-D15S159
123	in Ovariumorgewebe überexprimiert	ADP-ribosylation factor like 1	arf	12q22-q23.1	SHGC-12629; D12S1727-D12S78;; WI-7420; D12S346-D12S78
258	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 2			
259	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 3			

Seq. ID No.	Expression	Function
260	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 4
261	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 10
262	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 18
263	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 25
264	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 26
265	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 30
266	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 34
267	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 42
268	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 46
269	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 47
270	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 48
271	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 50
272	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 52
273	Overexpressed in ovarian tumor tissue	Lengthening to Seq. ID No. 56

Seq ID No.	Expression	Funktion	Module	Cytogetische Lokalisation	nearest marker
260	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 4			
261	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 10			
262	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 18			
263	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 25			
264	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 26			
265	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 30			
266	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 34			
267	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 42			
268	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 46			
269	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 47			
270	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 48			
271	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 50			
272	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 52			
273	in Ovariumorgewebe überexprimiert	Verlängerung zu Seq ID No: 56			



TABLE II

Seq. ID. No.

ORF Seq. ID. No.

Seq. ID. No.	ORF Seq. ID. No.	ORF Seq. ID. No.	ORF Seq. ID. No.	ORF Seq. ID. No.	ORF Seq. ID. No.	ORF Seq. ID. No.
1	124	125	126	127	128	129
2	130	131				
3	132					
4	133	134				
5	135					
6	136	137				
7	138	139				
8	140	141				
9	142	143				
10	144	145				
12	148	149				
13	150	151	152	153		
15	155	156	157			
16	158	159	160			
18	163	164				
19	165					
20	166	167				
21	168	169				
22	170	171	172			
23	173	174				
24	175	176				
25	177	178				
26	179					
27	180	181				
28	182	183	184			
29	185	186				
30	187	188				
31	189	190	191			
32	192	193	194	195	196	
33	197	198	199			
34	200	201				
35	202	203	204			
36	205	206	207	208		
38	210	211				
39	212	213	214	215		
40	216					
41	217	218				
42	219	220	221			
43	222	223	224	225		
44	226	227				
45	228	229	230	231	232	
46	233	234	235			
47	236	237	238			
48	239	240				
49	241	242				
50	243	244	245			
51	306	307				
52	246					
53	247	248	249			
54	250	251				

**Seq. ID. No.****ORF Seq. ID. No.**


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55	252	253	254
56	255	256	
57	257		
258	274	275	
259	276	277	
260	278	279	
261	280	281	
262	282	283	
263	284	285	
264	286	287	
265	288	289	
266	290	291	
267	292	293	
268	294	295	
269	296	297	
270	298	299	
271	300	301	
272	302	303	
273	304	305	

The inventive nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 of the determined candidate genes and the determined amino acid sequences Seq. ID Nos. 124-257 and 274-307 are described in the following sequence protocol.

**Sequence Protocol****(1) GENERAL INFORMATION:****(i) APPLICANT**

- (A) NAME: metaGen - Gesellschaft für Genomforschung  
mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

**(ii) TITLE OF INVENTION:** Human Nucleic Acid Sequences from  
Ovarian Tumor Tissue

**(iii) Number of sequences:** 284

**(iv) COMPUTER READABLE FORM:**

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25  
(EPO)

## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2434 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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cgggatttta ccgggtttta aaagcgaacc ttctcccggc tacaccggaa ggtacccaaa 60
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ataaattttc cagcggatta tggcattcct tccaggaaat acctcttggg aaaggcctgc 180
ttgcaaatat gcattttccaa acttgaaata taggtgtgaa cagtgtgtac cagtttaaag 240
ctttcacttc atttgtgttt ttttaattaag gatttagaag ttcccccaat tacaaactgg 300
ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac atggtcaact 360
gggacatggt aaactttgat ttgtcaaat ttatgctgtg tggaaacta actatatgta 420
ttttaactta gttttaatat ttctattttt ggggaaaaat cttttttcac ttctcatgat 480
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taaaactagac atcttaattg gtgaaagttg tttaaactac ttattgttgg taggcacatc 720
gtgtcaagtg aagtagtttt ataggtatgg gttttttctc ccccttcacc aggggtgggtg 780
gaataagttg atttggccaa tgtgtaatat ttaaactgtt ctgtaaaata agtgtctggc 840
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gccaccattt aacccttctt tgttctaaaa aaaaaaccaa agggcgctgg ttggtagggt 960
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ttggatctta tgatgctgag catgttctgc actggtgcta atgtctaata taattttata1620
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aactcatttc caaacatgta ccatgtttta taaacctctt gatttccagc aacatactat1800
agaaaaacac tgctactcaa aacacaactt ctcagtgtca tccattgctg tcgtgagaga1860
caacatagca atatctggta tgttgcaagc ttccaagata gcctgaactt aaaaagtgg1920
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tcatgctcac ttcttaaaag tcataaaaaa aatcaaatag gatcatgttt attgtcatgt2100
gtttcctggt ttctgacctg tgtgcacacc cctgtgtgtt tataattttt aaattgaatt2160
ttatatgggg tttttatttg ctaaaaacca ggctgttgaa tcacatttgg gaagggtact2220
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ggacttcttg ggatttaate taattgtcac ttcgttaggc agatgcactt ttttgataa2340
tggaaagtta agcataccga atgctacttt tgggtgacaa acgggcctaa tagtccgggg2400

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## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 798 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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gcctatattg gaagcagaca gcgatactga tgacattgac cacagagtta cagaggaaaag 60
ccatgaagag ccagcattcc agaattttat gcaagaatcg atggcacaat actggaagag120
aaacaataaa taggagactt tagcacactt cacttgtttc tagaagtcca gaattttgga180
cctccacgtg aaagaactgt ttttacctct gaactggggg ctcccataag ggataatttt240
cctcagagta gcaaagtttc tcttattaga gaaatcttgt gactcagatg aagtcaggga300
tagaagaccc ttggacctgg cagggttaatg ctgattattc cttggccttt cccttgatt360
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gaccacctca gatctctatt attaggctag atgtatagcc tctactcccc cagcttcttg540
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gcttatccag aacgggtggca gagtctcctt ggcaatcaac caacgttgct atgaaatatg660
cctcacactg tatagctcat tataggacgt caggtttggt gaaaaaagtg ggcaagacat720
gattaatgaa tcagaatcct gtttcattgg tgacttggat aaagactttt taattttaaa780
aaaaaaaaa aaaaaaaaaa
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798

## (2) INFORMATION ON SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 882 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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agaccttcca gcagtacttt ggtggacgag ttggagtcac ctttcgaggc ttgctttgca180
tctctggtga gtcaggacta tgtcaatggc accgatcagg aagaaattcg aaccggtgtt240
gatcagtgtg tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttaca300
aaaagattgc agttatctgt ccagaaacca gagcaagtta tcaaagagga tgtgtcagaa360
ctaaggaatg aattacagcg gaaagatgca ctagtcacga agcacttgac aaagctgagg420
cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagcccgc cgacatccct480
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cagggtcctt tggcctacct ggagcaggca tctgccaaca tcctgcacc tctgaagcca540
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acattccttc ctgtggactt gacatttttg aagaactctt tgccagataa tgagttcatt660
ttagttttat gctccattg aaaaattttc cactattttt ataagctgtt aatttcttga720
gtactttata acatgtctgt agcttgata aaccaagtaa gtattttttt tttgtcttta780
gcaaagttaa gactgtgaat atgatgacac agattctttt ttatggtggc tttgcttgtt840
ttaaattttt gcatgacttt taaaaaaaaa aaaaaaaaaa aa 882
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(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2901 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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actgagtcaa gatgaaatca ggacactgaa acagaaaaaa attgatgaaa cttctgagca 60
ggaacaaaaa cataaaagaaa ccaacaatag caatgctcag aaccccagcg aagaagaggg 120
tgaagggcaa gatgaggaca ttttacctct aacccttgaa gagaaggaaa acaaagaata 180
cctaaaaatct ctatttgaaa tcttgattct gatgggaaaag caaaacatac ctctggatgg 240
acatgaggct gatgaaatcc cagaaggtct ctttactcca gataactttc aggcactgct 300
ggagtgtcgg ataaattctg gtgaagaggt tctgagaaaag cggtttgaga caacagcagt 360
taacacgttg tttgttcaa aaacacagca gaggcagatg ctagagatct gtgagagctg 420
tattcgagaa gaaactctca gggaagtga agactcacac ttcttttcca ttatcactga 480
cgatgtagtg gacatagcag gggaagagca cctacctgtg ttggtgaggt ttggtgatga 540
atctcataac ctaagagagg aatttatagg cttcctgcct tatgaagccg atgcagaaat 600
tttggtctgt aaatttcaca ctatgataac tgagaagtgg ggattaaata tggagtattg 660
tctgtggcag gcttacattg tctctagtgg attttcttcc aaaaatgaaag ttggtgcttc 720
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tatgtggttg gcaaaatcag tacctgttat gggagtatct gttgcattag gaacaattga 840
ggaagtttgt tcttttttcc atcgatcacc acaactgctt ttagaacttg acaacgtaat 900
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tgatgtcttc tttgcggccg gtagcttgac tgagtgactg cattcactca acgaagtga1260
tggaataat tgaagtttat catgaatttt ggtttgagga agccacaaat ttggcaaccal320
aacttgatat tcaaagaaa ctccttgagg aattccgcag agctcaccag ggtaacttgg1380
aatctcagct aacctctgag agttactata aagaaaccct aagtgtccca acagtggagc1440
acattattca ggaacttaaa gatataattct cagaacagca cctcaaagct cttaaatgct1500

tatctctggt accctcagtc atgggacaac tcaaattcaa tacgtcggag gaacaccatg1560
ctgacatgta tagaagtgcac ttacccaatc ctgacacgct gtcagctgag cttcattgtt1620
ggagaatcaa atggaaacac agggggaaaag atatagagct tccgtccacc atctatgaag1680
ccctccacct gctgacatc aagtttttct ctaatgtgta tgcatgtctg aaggtcctgt1740
gtattcttcc tgtgatgaag gttgagaatg agcggtatga aaatggacga aagcgtctta1800
aagcatattt gaggaacact ttgacagacc aaagggtcaag taacttggct ttgcttaaca1860
taaaatttga tataaaacac gacctggatt taatgggtga cacatatatt aaactctata1920
caagtaagtc agagcttctt atttgatatt tggaagaaaa agccgtgaag tgtatgtaga2040
tcaaaaaatg gcttcttctt atttgatatt tggaagaaaa agccgtgaag tgtatgtaga2040
ccacttaate actaaatata tttgcctata ggactccatt gaatacatta gccattgata2100
atctacctgt ttaaatggcc cctgtttgaa ctctcaagct ttgaagacct acctgttctt2160
ccagaagaga acgttgaaaag tgccatgttt ctttttgctg gatctctgtt gatggcactc2220
tggaattgtt tcagttaagt cattttagac atagcattta ttatcactgt ggatctctac2280
ttggtgggtg ttatgaatc tttgaaagaaa tatattttga agaggtgtgg gaggaaggaa2340
tacattttat aaaaatgttg agtgaagccc acaattgacc tttgactaat aggagtttta2400
agtatgttaa aaatctatac tggacagtta caagaaatta cggagaaaaa gcttgtgagc2460
tcaccaaaca aggatttcag tgtagatttt gtctttcttg aacttaaaag aacaaatgac2520
aaagtttgaa tggaaaaagc tgctgttgtt ccacatctcg ttgctgttta cattcctttg2580
tggagcctac atcttcttaa gctttttagc aggtatatgt tgaacacttc tgtttcatgg2640
ttgagacaga atcagaggcc atggatactg acaactgatt tgtctgtttt tttctctgt2700
ctttttccat gactcttata tactgcctca tcttgattta taagcaaaac ctggaaaacc2760
tacaaaaata gtgtgtgtgt ttatctagaa aaatatggaa aatattgctg ttatttttgg2820
tgaagaaaaa caattttgta tagtttattt caatctaaat aaaatgtgaa ttttgtttta2880
aaaaaaaaa aaaaaaaaaa a
2901

```

## (2) INFORMATION ON SEQ ID NO. 5:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 579 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

aaagaaagag aaagaaagaa aagaagattg tagctagggg gagagtaggt gaaaagatga 60
acaacatgac cgggaagatt tcctaattct accacagcct ggctctacct taagtctttal20
ataaaaagctt gactgaaggt accaaggtgt gctgaagtgg aagcaaagtt ctccaaagtc180
cagcatggta gacatcagtg gtggtaacca aggacagacc ccaaggcaag gtgaacctca240
aaaatggaac ctcaagtcta tgcagtccag ctgccctccc caccagaaaag tccttggtcc300
agcccaacat cagtgcctct gagtttggtt actagaaaca aaggaagaat ttccttgtaa360

aaatatagac agagtagtcc ctggctttct cctcttgacag gaaggatgga ttctccatt420
ccataccatc tttccccac actggcccca gaaataactta attcaactat gtgaaaataa480
agattgtttt tggtttgagg gcatagggat ccatttatcc ttattcttta tgaggcacta540
aattagcttt gtatgttatt aaatgtgtct cgtcaatgc 579

```

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2809 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gcagggcctc gtgccgtttg cataaatagg tttctcact cttctttttt tccttctttt 60
atccctcact ccctccccta aacctgctt cagcacaatg gactaattct agcattctga 120
tcataaggcc ctccattttc ctaatgtgtt tcaaggaatc tttttaggaa aaatatccag 180
attattcatt cacttttttt agtatctact aacaactcct tttttctctt agagagttaa 240
gaaggaacag gttgtccttg tctggagtca agctaaacac atgatttggt ttatcagcag 300
ctggagcaga agttgaaatg gtctttctgt gagacagtaa tttgctactg aagctttatg 360
gcttgtttgc actgattact ccaggatcca aaaacttggt gaaagtcact gaaacactca 420
aggcaaatca ctttacagcc ctgagtgtct gtcaccatag tttgcataat gaatatgaat 480
cccattgggt tgtgatgtag gaaatcctgt agttgtattt tcttgaactg aaatatttga 540
ctcaaaataa ttaagactca ttgtcatttt tcatcttggt attattgtgg acaagttgac 600
atattaaatc tctttgcttt ctggttaagct tagcttttaa aatgcatttt cccttgctct 660
gtctttaact agatatacat gcttatattt atagtgggtt tcacagacta taaaattgaa 720
tgtatgaaat ttttatttat atcagtgttt ttaataatga agatattttt ggagtaatgg 780
tgctgtcttg tagcgagtta ttaatcatag taagattttt ttctcttcat ttgctttttt 840
tgtttcatat taacaatttt ttttttacac ggacacaacc ctctgacagt ctttccaaat 900
attaaaatca tttgaatatg tatgctgtga tctgaacact gctcaagcca tcaagcagtc 960
ttcatacagt ttgcattata aaatctcatt aaattctcca agaaaaata agttgaagaa1020
ttttatttcc tgaccatgca tcccctggat ttctgagttt cagttcagat tgtagatgac1080
aatataagct gccttccgaa attgtcaaca tctgaatgtt aagtcatttt tccccatgg1140
agaagcccggt agttccatga agtatggatt accatttgta tttttcacta acagtaaatg1200
tatttttctt attaatgttt tgcccttagga atgatgaatt acattttttt ttccttctta1260
ccataaacat ctgcattcct cagctcagcc ttccttgatg gttgtttctt tataaatgg1320
tgagctgctg atgcagggtat tgccaagcta acagtacaaa tcattttaaa gaggaagctg1380
gcgcgtatgg cagccgagga gcacactctg caggacactg gacaagacag taaatattca1440
acttttaatg ctgattaaag gagtataggt aaagaatacg taggtataca taattgggtg1500
gacaaatatt cactttattt atattttata tattattttt ttaatttggt aaatactatc1560
cagtttttga gttgtccttg ttgatttggt tgatattaaa gtattagtaa taattgccag1620

gaaactatca ttagggaggg tttagtgggt tgctgtttgg actgggaggg atgatttaaa1680
tttagtgcta gaaaccaatt ttagtgactg cacagttaa ctttgtcag acagaaggt1740
gctataaagc taccctgtaa gtcatatcaa aaaagttcag aggaagatta gtaaatattt1800
atcaataaaa ataaacattt tgtttttcta atatcttaac atatctctcc ctttaggagg1860
aagaacgtgc aaaacgtgag gagctagagc gaatactgga agagaataac cgaaaaattg1920
cagaagcaca agccaaactg gccgaagaac agttgagaat tgttgaagaa caaagaaag1980
ttcatgagga aaggatgaaa ctagaacaag aacgacaacg tcaacaaaaa gaagaacaaa2040
aaattatcct gggcaagggg aagtcagagg caaaactgtc cttctcatta aaaaccagg2100
attaaattgc aaactctgaa ctttttacia agaaaaatgg aaaaactttg tatggtagct2160
tcatgttgaa gtggtttttt gtttttggtt ttgttttttt aatttgtaaa atctggaaag2220
ttagcttggt ctaatagggg ctatgctctg caattccctt tttttttttt ttttttctt2280
ccactaagtc aaatccttat cagatcattg ttgtattcta aggagtgcag tatttttcac2340
ctgtttggat tctatattag tggctcgagg aagagcagat cacattgtaa aactatggat2400
ggtctgataa ggtctttact gaccccaact acttcagagt tatactctgt ttgctacatc2460
ataatgctgg ttttgctgac tttttgtttt ttatatattt tataaaaaaa gaaaaagttg2520
gtgatgtcat tgggaaattc ccagggtatt actggacctt tgtggtgtat tgttaaacca2580
gtgtccttgt gatactgttg ctcttgatgt tcttgatata ggtaaggaaa cagttgggtca2640
actctgatac aaagtatata tacagttcag tattgtctct gttcattttg tttttatttc2700
attgacaaaa tcaaacaccagc attccccatt gtgtaataaa atgattttgc tgaataaagt2760
aaagtcttaa attcaaaaaa aaaaaaaaaa gaaaaacaaa aaaaaaaaaa 2809

```

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 910 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

```

agttcggcac agagaaagta ttttaaccta cctgtagaga tcctcgcat ggaaagggtgc 60
caaaactgttt tgaatggaag gacaagtaag agtgaggcca cagttcccac cacacgagg120
cttttgattt gttctacttt ttcagccctt tactttctgg ctgaagcatc cccttgagg180
gccatgtata agttgggcta ttagagttca tggaacatag aacaaccatg aatgagtggc240
atgatccgtg cttaatgata aagtgttact tatctaataa tcctctagaa agaaccctgt300
tagatcttgg tttgtgataa aaatataaag acagaagaca tgaggaaaaa caaaagggtt360
gaggaaatca ggcataatgac tttataacta acatcagatc ttttctataa tatcctacta420
ctttgggttt cctagctcca taccacacac cttaaaccctgt attatgaatt acatattaca480
aagtcataaa tgtgccatat ggatatacag tacattctag ttggaatcgt ttactctgct540
agaatttagg tgtgagattt tttgtttccc aggtatagca ggcttatgtt tgggtggcatt600
aaatttggtt ctttaaaatg ctttggtggc acttttgtaa acagattgct tctagattgt660
tacaaaccaa gcctaagaca catctgtgaa tacttagatt tgtagcttaa tcacattcta720

gacttgtgag ttgaatgaca aagcagttga acaaaaatta tggcatttaa gaatttaaca780
tgtcttagct gtaaaaatga gaaagtgttg gttgggttta aaatctggta actccatgat840
gaaaaagaaat ttattttata cgtgttatgt ctctaataaa gtattcattt gataaaaaaa900
aaaaaaaaaa

```

910

## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1447 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

gcgacggcgg cttagaaagt gcttcctgga ggcgacagca ggatcatgaat catgtgacgg 60
tggtcttgagg aggaacctgt ctttaaagct gtccctgaag tgacagcggg gagaaccagg 120
cagcccagaa accccaggcg tggagattga tccctgcgaga gaaggggggt catcatggcg 180
gatgacctaa agcgattctt gtataaaaag ttaccaagtg ttgaagggtt ccatgccatt 240
gttgtgtcag atagagatgg agtacctgtt attaaagtgg caaatgacaa tgctccagag 300
catgctttgc gacctggttt cttatccact tttgcccttg caacagacca aggaagcaaa 360
cttggacttt ccaaaaataa aagtatcatc tgttactata acacctacca ggtggttcaa 420
tttaatcggt tacctttggt ggtgagtttc atagccagca gcagtgcgca tacaggacta 480
attgtcagcc tagaaaagga acttgctcca ttgtttgaag aactgagaca agttgtggaa 540
gtttcttaat ctgacagtgg ttccagtgtg taccttatct tcattataac aacacaatat 600
caatccagca atcttttagac tacaataata cttttatcca tgtgtcgaag aaagggtccc 660
ttttccaac ttatactaaa gagctagcat atagatgtaa tttatagata gatcagttgc 720
tataatttct ggtgtagggt ctttcttatt tagtgagatc tagggatacc acagaaatgg 780
ttcagttctat cacagctccc atggagttag tctggtcacc agatatggat gagagattct 840
attcagtgga tcagaatcaa actggtacat tgatccactt gagccgttaa gtgctgcaa 900
ttgtacaata tgcccaggct tgcagaataa agccaacttt ttattgtgaa taataataag 960
gacatatatt tcttcagatt atgttttatt tctttgcatt gagtgaggaa cataaaatgg1020
cttggtaaaa gtaataaaaat cagtacaatc actaactttc ctttgtacat attattttgc1080
agtatagatg aatattacta atcagtttga ttattctcag aggggtgctgc tctttaatga1140
aaatgaaaaa tatagcta atgtttttcct caaactctgc tttctgtaac caatcagtg1200
tttaatgttt gtgtgttctt cataaaattt aaatacaatt cgttattctg tttccaatgt1260
tagtatgtat gtaaacaatga tagtacagcc atttttttca tatgtgagta aaaataaaat1320
agtattttta aaaatataaa aaaaaaaaaa aaaaaataat ttttttgttc agactttttc1380
caaaaatcta aacataatta atatactctt tcagccacat gaataaataa tgagtgtttc1440
ttgtaaa
1447

```

(2) INFORMATION ON SEQ ID NO. 9:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 671 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

agcgcggtga agcgggggtg ggatctgaac atggcgggcg tggtagctgc tacggcgctg 60
aagggccggg gggcgagaaa tgcccgcgtc ctccggggga ttctcgcagg agccacagct120
aacaaggctt ctcataacag gaccggggcc ctgcaaagcc acagctcccc agagggcaag180
gaggaacctg aacccctatc cccggagctg gaatacattc ccagaaaagag gggcaagaac240
cccatgaaag ctgtgggact ggctggggcc atcggcttcc cttgtggtat cctcctcttc300
atcctcacca agcgggaagt ggacaaggac cgtgtgaagc agatgaaggc tcggcagaac360
atgcggttgt ccaacacggg cgagtatgag agccagaggt tcagggcttc ctcccagagt420
gccccgtccc ctgatgttgg gtctgggggtg cagacctgag gagcgctgcg accctcctag480
gctattgact gttaagtcct caggtttggc ccagattcca gttcgtgcct ctgaggtcca540
ccagagggcg catgaagccc aggctgttgc caaacctac cctgccccac accaaggagc600
ccaccaaagg caaataaagt tattgagtgt ttagtagaaa ggaaaaaaaa aaaaaaaaaa660
aaaagtcgac c

```

671

## (2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 803 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```

gaagatgagg tggagaaga gtcaacagct ttgcaaaaaa ctgacaaaaa ggaaattttg 60
aaaaaatcag agaaagatac aaattctaaa gtaaaaccca aaggcaaaagt tcgatggact120
ggttctcgga cacgtggcag atggaaatat tccagcaatg atgaaagtga agggctctggc180
agtgaaaaat catctgcagc ttcagaagag gaggaagaaa aggaaagtga agaagccatc240
ctagcagatg atgatgaacc atgcaaaaaa tgtggccttc caaaccatcc tgagctaatt300
cttctgtgtg actcttgcca tagtggtatc catactgcct gccttcgccc tcctctgatg360
atcatcccag atggagaatg gttctgcccc ccttgccaac ataaactgct ctgtgaaaaa420
ttagaggaaac agttgcagga tttggatgtt gccttaaaga agaaagagcg tggcgaacga480
agaaaagaac gcttggtgta tgttggtatc agtattgaaa acatcattcc tccacaagag540
ccagactttt ctgaagatca agaagaaaaa aaaaaagatt caaaaaaatc caaagcaaac600
ttgcttgaaa ggagggtcaac aagaacaagg aaatgtataa gctacagatt tgatgagttt660
gatgaagcaa ttgatgaagc tattgaagat gacatcaaag aagccgatgg aggaggagtt720
ggccgaggaa aagatatctc caccatcaca ggtcatcgtg ggaaagacat ctctactatt780
ttggatgaaa aaataataac ggc
803

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 828 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

agcattcca ggctgggggtg tttgtttgga ctggagaagg gaggcggcgg gccaaggcac 60
gtcgagcggg ggagcggcgc tgctgtgga gatccgcgga ggccgacagg attcgttggc120
tgccgtcccc gctgctgtgc attgggttaa aaacgacaac caacatcagc catgaaagat180
ccaagtgcga gcagtactag cccaagcatc atcaatgaag atgtgattat taacggtcat240
tctcatgaag atgacaatcc atttgacagag tacatgtgga tggaaaatga agaagaattc300
aacagacaaa tagaagagga gttatgggaa gaagaattta ttgaacgctg tttccaagaa360
atgctggaag aggaagaaga gcatgaatgg tttattccag ctcgagatct cccacaaact420
atggacaaa tccaagacca gtttaatgac cttgttatca gtgatggctc ttctctggaa480
gatctgtgtg tcaagagcaa tctgaatcca aatgcaaagg agtttgttcc tgggggtgaag540

tacggaaata tttgagtaga cggggccctc ttttggtgga ttagcacaa tttccacact600
gtgaaggcag tattagaaga cttaattgta aaagctctct tgtaactgtg ttacacttat660
gcattgccaa agtttttgtt agtcttgcat gcttaataaa agtgctgaga cacttggttac720
ctaagtaaaa agcctgggtc aaaccatttt actgggaaaa taggattggg gccccatggc780
cttggtgtgt ggaagaccgc caaggggaag gaaccaccag gcccaagt
828

```

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 552 base pairs
- (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

ttggtttccg ggcgccaacca atgtggggagc tgtaatagta agagcttcct aaccaaagct 60
tggattacc gtgtggggtt tcgttttttt cgtgggtggt tatttgattt tgattttttt120
ttcttttatg tgatcttttg gaaaacacat tcagaattat atctcgtttc tacttaaatg180
tagtgcttag ggtaattttt ttgtactgaa gtctttattg gtgggtgcat gctactggga240
acaagttttt gtacaaaagc ttcaatcaga atcactgtgc attactgaga ctctgtttat300
cactagcctt ctgtccctcc cgcagaagac tgttggtatt aacaaaataa tatgtatttt360
gatttactta aagtgccttg aaatttctta gggacctgcc acttttgact gtggatcagt420
tgatgtacac ttgtattatt aaagcactca ataaatcact gtggctgata actgcaaaaa480
tggaaccg acatttgctt tgtgtcctgg tgaccgctgt agccctacgt gcagtggagc540
cttgtctaat tc

```

552

## (2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 993 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

gcggtattaa tatttaattt atttttttta cttataggto atgttgatgt ctatgataaa 60
cagatgtttt gcctctgaca gcagaacttc ctttcatttt tctcattcgt tttctttggt120
gggttcattt ttttgaatca accacacttc attattttcta ttaagcaatt tgacaggact180
gttgtagcct gcagtgtagt aaaccttctc atcgaaaact tttccatctt cccttaaaat240
gcttgctaag gtcaaaagtt gttcttgatt cttttgggca ctagaaaatc catcgaaaaga300
ccgtacaaaac acagtcattt cggctctatc ttcaatgaag acatctgact cttaaaggcct360
gggtggatca aattgctgtt cagagggaat atacagggaa atggtaatgg tagactcact420
aaaaggacct gaaccaggct ccacgtagct tgtcactgga gctgtcatct ttattttcat480
ctctttctcg tttttgcctt gaatgtagct gttcagtttc gtaaagcccg tctggatggc540
tgaatcccag tccatagact ccacggacgt gctgaccac ttggctggtc catagtgtcg600
gatctcataa cttccgggct gggggccggc gtcctccggg gccttcacgc ccggcgctc660
cacagcttgg gcgcgcgct cctcgccgc cccggggtct ggctggagcg gctcgccat720
gggcggcggt acgctctggg agcctggtca gccgcgcaga ggccccgcac ccggggccgc780
cccgcctgcg tgtgcgcgcc ccgcgcaggg cccgagtcct cctccgcaga ccgggtccct840
cctcccggcc gggctggaga cccgagccca cccgatgcgt ctgcctctgg accgcgagg900
ggcgccgcca ccaaggcggg gccggctcac gaccccgac agctccggcc ggagttgcgc960
gtcctgcccc cgcccccccg cggcgacagg gag

```

993

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ctgcacctta gaaaaaaaaa gaaaaatcaa aaaaacaaaa aaacaaaaac aaaaaaagaa 60
ggaaaaatctt ggagggtggg cgtgggaact caggacccca gagtggcgag tgggtggtggg 120
agggagagacc tctctccccc tttctgtgtg gagaggaact cttagtgtct ggtgcagcta 180
ttaaattgtc aatgtgtcaa gtagcttgtt ttacacgcta caacatagct catttgtaac 240
ccattgtata agctgtgtat ttacaaatat aacacaacaa ttttaactttt ccttagaata 300
caaaaaagtca tgcattgtct ggggaactat atgcttttcc atttttaagt caggactgca 360
atactgattc cagttaatga gcagctaaga tccaatctgt ctaatacagt gaccccttag 420
ccatccgggc ctggcaatat acaatttttt ttcccctcca agtttgaac actcccttc 480
cagaaaggca ttgtgcaaca caggattatt tttaaatgat tctgaatttg aattaacttt 540
ttggagaatt ctgtgatgcc cttagaagaa attggacacg tattgagtgt cacaaagctg 600
gggctgggaa ttgctgtgtc aatgtttcat tagacttaag aacctaaaat ttttctcagt 660
tgggtggata aaaccactaa cgcttagaaa ctgttttctc atgcagctat gtttctctta 720
tttatgcctt gaggactaat ttctgttttt ctactgttta atgcactgtt gaccttcata 780
atgggtgcctt acgcaagcga tcccttctgt ggggttctca tacaggggtg tgggcgagtc 840
atgctttatt aaggctcttg ttccacctgg cagtgtactg tatcaacgta taatacagaa 900
aaaaaatctc ttttaaggctc tccctcacaa agacatagag tgaactccc tttacatgct 960
agtatttgtt caacacttta ggcaacttga ctgtcagtgt taaaatggaa aacaggaaaaa1020
tggaaaaaatc tgaccaatctc tgccaccttg agactttcat atagaccttg cacaacaatt1080
gtatagatca cacaccggct gtatttaata tghtaacattt tcacacatat taaagatacal1140
gaagtattaa aaaacccccca atgttaatgt atttgcttaa aaggcacaag ttccacatat1200
ctgtctagct atctgttggt aatacagaaa gtatactact tttttaaaaa agtgggcagaa1260
attcttgtgt atgtatattt gtgtgtacag tatgtgtatg tgtgtatata tatatattat1320
atatatagat aatatataaa tatttttttt aaggagaaac tagaatgttt agctagaaaaa1380
ttccacagcc tgtgaagaaa tatttcaaaa tggccataaa ggaggtaaaa atgaaaaccal1440
taacctaaact tttatagagg ctttatcttt aatttaacga tgtgcggagg actttcttgc1500
ttgaatctgt tccgggctgt ctgctctgtc catcaaatgg gcaggctctg aatggggcac1560
cttcggccgt tcagaagtgg cctgaacaga atgctggaac ccaggctgga ctcggaacac1620
ctaaggtttt gattttgaat ttcagcctta ttagaagatc taacctaaaga gtaagctaac1680
cacagggtatt cttttgtaga acacttttta tgcagatgaa gctatttttt ccagcaagtal1740
gattcttcca gtttttccaa ggagtaattt ccccgaaattg gcataccacg gcgtggacag1800
ctgatatctc acccagctgc tggcttgtgg gtgtggctct ttgctttata tatatataca1860
cacatgtgag tctggctggg ctggtatttt gtttgatctt cctggaaatg agcagtgaact1920
aacgctcaca taactggttt tttttttatc tgggctgatg aatacattta cctaagaaaa1980
tcatttcgtt ttacttaaga ggggaagtgc agttttcttt tggcagttca gaatccaagc2040
acttgatttg ctgggtttgg aaaactcctt ttttggcctt ctatgtgctt agccataaca2100
attccattaa gcaagaaggt aagcaaaaaga caaaaaaaaa aaagggaaaa aaaaaaaact2160
tgcacgggct tgtctcactt acgaaacatg tggagctgt ttgcctgggt ggggctgggt2220
accgtacctg tcaatgcctg ggattttcca taaatttagc acgggacata aag 2273

```

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 986 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```
gcgcgatata aacagttgga agagaaaatg gtacagcagt tacaagagga tgtggacatg 60
gaagatgctc cttaaaaatc tctgtaacca ttctctttat gtacatttga aaatgccctt120
tggatacttg gaactgctaa attattttat tttttacata aggtcactta aatgaaaagc180
gattaaaaga catctttcct gcattgccat ctacataata tcagatatta cggatgttag240
attgcatctc agtggttaaat ctttactgat agatgtactt aagtaaatca tgaaaattct300
acttgtaact atagaagtga attgtggacg taaaaatgggt gtgctatattg gataatggca360
ctaggcagca tttgtatagt aactaatggc aaaaattcat ggctagtgtat gtataaaaata420
aaatattctt tgcagtaaaa tattcccttt gttaatgtta tagaaggggg gatacaaaaa480
ggaactaaca atttgtatgg cagtgtcaga tatttttatt ttagtatttc ctgttttgg540
ttatttgcat cttagaagag cataatgaca ttgtttgatg aagcctaatt atgctggact600
gttttgacct ggtttaaccc ttctgatagg tagttgtgga tgctggggat gagaactgaa660
taattcttgc ctggagtgc actacactct agaatttcca ctttggagaa tactcagttc720
caacttgtag ttctgatag aacagacttt acttttctag cccagcattg atctagaagc780
agagggaatcc cagcgccctt taaaagtgtg tatgtgggtt tcttttaaaa agctcctgtt840
tttggaaagt agaatttatg ggtacaacgt atgttcatta tttgtacata aaataaaaacc900
atttaaaaag ttaaaaaaga aaaaaaaaaa gggggaaaaa aaaagagaaa aaggaaaagg960
aaaaagaaaa aggaggggag aagaga                                     986
```

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 526 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

gcgtctatat tacatttatt gacactggat atttattatc tgttatatac caggcaaaat 60
ggacacacca tcaggagata agacctgtat cttacgtgta agatgaaact tatgcaaaaag120
gcacagaaca aattatttgg tcacagttac ttttaactct ttcagcaatg cctgagtcct180
ctttatagaa acttcatttt gctaagttag caaccattca tttttttggt tactcttcat240
gtatagtttt ctcaagtgtc tcttcaaata ctgcataatg gtatagacca tttaatatc300
caaacataat ctgaaagact agaggaatcg ccattaattt catttgtgtt tgacaaagcg360
tcatccaatg gattaaaacc cttccttttg gtggcagtg aacggtatga tacctaaaaa420

gaaaaaagag ttaatcacct ctctggata tgaatgctat tagaagtttg ttgactttctc480
ctaaattgat aattgccttt ctagatctat aatgtagaga gcaaaa 526

```

## (2) INFORMATION ON SEQ ID NO. 20:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1765 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

tttttttttt tttttttttt gctgtttttt atttatattt gatgtgtgtc aaataataat 60
tttttttaaa aaaatctcaa aacatgttca aacacattca gtagcaaaaga tccaccattg 120
gcacacacat taagaaagca cacacactag gcttctagtt gggctaatta aaatctctat 180
gggtggaaag gtggttggtt gtacttaatt aagctttttt gaagtgcataa gctatgcata 240
acagatgagc ttgaaagctg cagagttaa gatagactta atttttcatg attttcccaa 300
agccagtcac gatatttatt taatttgtgg tcttcagggt gcaccaatcc catgaagctc 360
aattggatac ttccactgct ttgtcaggta ttcactgtgag aacttgacaa tggtttttgc 420
ccgaagatcg tagagacca gaggtttaag aagtcttgac acatctctcc agtctgcggg 480
tcttgctacc tcagctgaag gatacttctc cagaaacttc caaagcacag gtattgccat 540
tttgctgag gtccgattga gaaatatagt agcgatgaga agcttccatg gatcatgaaa 600
aagtgtttct tgaacgagat taaaagggtga ccgaggaggt gtccatttct taaaggcttt 660
acgtcgtagg gggctaagag cttctttgtt atatttgcgt gaaaaataca ggcttggttt 720
ccttctttct atctgtgttc gtgggatggg atcttcagtg aagtctttcc tggttggtga 780
gcagtgtttg tccatttcag agccacgttt taaaatgtca gtatgcaaat gttctttcct 840
ttccacaact tctactttg ttccgatttc ttcagattct aaaaagggtat cctcataact 900
ctcgttgtgt tctgagcttt tggctgaaca aaatttgttt atgatgccag aagttttttg 960
ttcagaacaa aaatttgatc ctgaactcaa tgatctttct ttttttttta caaggctgtt1020
ttcttcaactg gtcacactga gggctctacc acatgtctca gcatcagaaa tgcagacagt1080
tctatcaagc tgactttttt gtgcaacagg ttcactttca gcatctgctt tattacacac1140
agattctctt ttgctatcac ttggaacaaa acctgaacag ctcttctctac atcctttttt1200
agttttctta attgggattc ctttcaaaat agtcaccttt cctttgggct ttctaacctt1260
tctgaagtta acatcatcaa caccctcacc ttctttcaaa agcaaatgag tgggaagtaa1320
gttagagagt cctctgctct cctgcaactc tgaactacta cttggcggca taaacacatc1380
ctttttgcac ttgcttcggg tcttgaggtt ccagtttgaa ttgttacttt ggtttttagt1440
atgggatgtc agggctgcca tgctgcagtc tttatatctt gacttgatac cccttttaga1500
aagtacagta aaatcaaaat cttctggctt aagagaagtc tctccatttt tgtgaagata1560
attagcaagt gaacttttgg atctgaactt cagtccttgt gggctagaaa atgatattaa1620
agggaaactta ctgctagtaa atagaaggga cttttaaaag aactggacca catttcagat1680
ttctaattaa ttccaaaatg ttgccatagg tatctgtcat taaaaaatga aaaagagtga1740

```

taaatggcac ttttaaatgg tttcc

1765

## (2) INFORMATION ON SEQ ID NO. 21:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 746 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

gttttttttt gttttcttta aatttgatg tctctacacc actcctgatt tgtaggacta 60
aatagatcta tttattccaa tgcaaattgt gtaacattta tttcttcctt gatttttaaa120
aatatcttag tattottaac tatgtatgtg ccttctctta cactgagttc ttttttgctc180
ctttcagctg ctacacacaat cctgtctgtt ggagtcatag ctgctaattc catattatatt240
ctctacacac ctggaacatt tagtgtatta ctggtaccct tctgtgttct aggaaacaaa300
tgaattgcaa actggacttg taacaggatc atacatagag caacaaatta gctactggct360
ttgtaagata gtaagttagg aatttcacag tcatgtctcc aaatttcatt gcagagttaa420
aaaaacaata taagactgtg gtaaggtaca aacgcaaatt caatttgctg tgactaattt480
cctaggactt atttccttat gtaaaacccc tgttctttct ttctgcccac aagacagggt540
acaaagcttt ctaaaacatg ctctcaggtg tccacacctg agacattgct ttgtggatac600
totcaaaggt gtccacaaag caaaaaaatc agaccaaatg ctaagagcaa gtaacttata660
cctcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaattgttt720
tgctaaatta ctaaaataat agccgc
746

```

(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

agcagactca caccagaact acattccctg gccccctgcc tgtgtgcttc tggccaggcc 60
ttgggttggca agtctgaccc gagaaaagga tctgcagaaa atcagactat gggatcactt120
tgttttgtgca ttgggaatga cattctttcc caccocagga aaaccttttg gactttcaga180
gacatttgtg ctagccaacc acatgggtcag cctcaaagtt gagagggtca gtaaccctcc240
tatccctaga gaattccaaa gtgtggatgt aatttaacta gaaagccatt ggtgactatc300
tgtgatcttc tggaaagtat ctatgtttgt tatatottgc atccaaagcc agaggggaacc360
acaatgacta gtaaaacggg ggtctcaatg cccacttagc ctctgctctt gaatttgacc420
atagtggcgt tcagctgata gagcgggaag aagaaatatg cattttttat gaaaaataa480
atatccaaga gaagatgaaa ctaaatggag aaattgaaat acatctactg gaagaaaaga540
tccaattcct gaaaatgaag attgctgaga agcaaagaca aatttgtgtg acccagaaat600
tactgccagc caagagggtc ctggatgccg acctagctgt gctccaaatt cagttttca 659

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 357 base pairs
- (B) TYPE: Nucleic acid

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

cgccagtgcgc agccgtgggg ctctctcctt gtcagtcggc gccgcgtgcg ggctggtggc 60
tctgtggcag cggcggcggc aggactccgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgccc ttctccctgg agtaccgagt ctctctcaaa aatgagaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcacccct gtttttggac240
acagtctctt tactcagatc agctagttct acatatgaat tttcttatat gtctctcaac300
aagtgcctaa aatgcctcgt tgtgctgtga gtaaaggctt gttgattagg ctgggcg 357

```

(2) INFORMATION ON SEQ ID NO. 24:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 890 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

cggaggcagc ggaaagccga gccaggcgcc tgcgcgctgg gaagagtagg ttcagagtgc 60
attccggaac ccggggcgcg gcgcactgcg caggcgggcg gactccgctc agtttccggt120
gcggcggaaca ccaaagtcgg ggaacttaag cattttcggg ttctagggtt gttacgaagc180
tgcaggagcg agatggaggt ggacgcaccg ggtggtgatg gtcgagatgg tctccgggag240
cggcgagggt ttagcgaggg agggaggcag aacttcgatg tgaggcctca gtctggggca300
aatgggcttc ccaaacactc ctactggttg gacctctggc tttcatcct tttcgatgtg360
gtgggtgttcc tctttgtgta ttttttgcca tgacttggtc gctgatctt aaattaagaa420
gttgggttctt gagtgaattc tgaaaatggc tacaaacttc ttgaataaag aagacaggac480
tctcaataga agaatttcac atctccaagg gaccttctt ttcattttac actttgttac540
taatttgcag aactctatta attgggtagg atttcaccca ttcctagcta agttcttaaa600
attaaacctt ttgggtcgtg tttaaaaact ttcaaacatc tgatggcttt acaggggctg660
aatataaaag cattgttact taaaggctct gtgtattcat taagaaatat agtaatgtct720
tttaaatgtt taagagttga tcagggttta ctatggatgg caagtaatag ggatgattaa780
taaggggag agttttatgg aatttcaaaa gtcaatttat ttcaaaagcg ggggaaaggg840
ttttgagagg agggggggccc aaggtgttcc tggggtttgc cgaggggaggc 890

```

(2) INFORMATION ON SEQ ID NO. 25:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 651 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

gccgtatatt gcatactaca tcagcaaaaag gtgttgccggc tttataagcg ggcgctacgc 60
cactctgagt cgtggtgctg ccagagagac aaataccgat accttgcttg tttgatgaga120
gcccgggtttg aagaacataa gaatgaaaag gatattggcga aggccaccca gctgctgaag180
gaggccgagg aagaattctg gtaccgtcag catccacagc catacatctt cctgactct240
cctgggggga cctcctatga gagatacgat tgctacaagg tcccagaatg gtgcttagat300
gactggcctc tttctgagaa ggcaatgtat cctgattact ttgccaagag agaacagtgg360
aaaaaaactgc ggaggggaaa ctgggaacga gaggttaagc agctgcagga ggaaacgcca420
cctgggtggc ctttaactga agctttgccc cctgcccga aggaagggtga tttgccccca480
cctgggtggc atattgtgac cagaccccgg gagcgcccca tgtagaaa gaagagacct540
atctttcatg cttgcaagtg aaatatgtta cagaacatgc acctgccta ataaaaaat600
agtgaatagg taaaaaaaaa agtgccattg tagtatgcaa taataagcgg c 651

```

## (2) INFORMATION ON SEQ ID NO. 26:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1256 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

ctcgagccga attcggtctg agctttcatc tgaccatcca tatccaatgt tctcatttaa 60
acattaccca gcatcattgt ttataatcag aaactctggt ccttctgtct ggtggcactt 120
agagtctttt gtgccataat gcagcagtat ggaggaggga ttttatggag aaatggggat 180
agtcttcatg accacaaata aataaaggaa aactaagctg cattgtgggt tttgaaaagg 240
ttattatact tcttaacaat tcttttttca gggacttttc tagctgtatg actgttactt 300

aaactatcta aaatagagca ttttgggtatc ttcatctga ccaccatat ccaatgttct 360
catttaaaaca ttaccacagca tcattgttta taatcagaaa ctctggctct tctgtctggt 420
ggcactttaga gtctttttgtg ccataatgca gcagtatgga gggaggatct tatggagaaa 480
tggggatagt cttcatgacc acaataaat aaaggaaaac taagctgcat tgtgggtttt 540
gaaaaggcta ttatacttct taacaattct ttttttcagg gacttttcta gctgtatgac 600
tgttaacttga ccttctttga aaagcattcc caaaatgctc tatttttagat agattaacat 660
taaccaacat aatttttttt agatcgagtc agcataaatt tctaagtcag cctctagtcg 720
tggttcatct ctttcacctg cattttatct ggtgtttgtc tgaagaaagg aaagaggaaa 780
gcaaatacga attgtactat ttgtaccaa tctttgggat tcattggcaa ataatttcag 840
tgttgtgtat tattaatatg aaaaaaaaaa tttgttttcc taggttgaag gtctaattga 900
taagtttgac ttatgatgac catttatgca ctttcaaatg aatttgcttt caaaataaat 960
gaagagcagc tgtccttctt tctcttttta agtgttcagc tgtggcatgc tcagagggtt 1020
ctgctggatt ccagctggag cgggtgtgata ccttctttt tcagctgttc gtgcttctt 1080
ttcttgtatc caccaaagtg gagacaaata catgatctca aagatacaca gtacctactt 1140
aattccagct gatgggagac caaagaattt gcaagtggat ggtttggtat cactgtaaat 1200
aaaaagaggg cctgggaatt cttgcgattc catctctaaa aaaaaaaaaa aaaaaa 1256

```

## (2) INFORMATION ON SEQ ID NO. 27:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 694 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtttctaaag gatgtgtaag aaaccagagg taaaggcttc gcgatatctt aagacatccg 60
gcgtagtacg cttcagtgag ccacagcgct agagaagtag gagaagctcg cgagatctgt120
gccgttgccg aggagactag gagggggagg agaggggatc tcgcgaaaag aaagaggtcg180
ggagcgctcg cgagatctcg gaccacccaa cctgaaaggt gcttaggaag ttgaaaggcc240
cagaggaggc ctccggggcaa atggccggag ctggaccgac catgctgcta cgagaagaga300
atggctgttg cagtcggcgt cagagcagct ccagtgtctg ggattcggac ggagagcgcg360
aggactcggc ggctgagcgc gcccgacagc agctagaggc gctgctcaac aagactatgc420
gcattcgcat gacagatgga cggacactgg tcggctgctt cctctgcaact gaccgtgact480
gcaatgtcat cctgggctcg gcgcaggagt tcctcaagcc gtcggattcc ttctctgccg540
gggagccccc tgtgctgggc ctggccatgg taccggaca ccacatcggt tccattgagg600
tgcagaggga gagtctgacc gggcctcgt atctctgacc acgatggcgc ttacctttca660
gacttcatta aacttatgac cgaaaaaaaa aaaa                                     694

```

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1927 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

gogagtattt attttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
agcctgttta acttttgata caaagtaaca ttttagtaca gaaaatccca gtctgtcagc 120
tcagtacctg tctgtgcaca ctgtaccatc tcagtcccac tctgcctgta acttagaaaa 180
cagcccttac ccccagaggg tctgcgagtt aataccttga gaatagtcta cagtttttca 240
tagtttgtct gagctagaaa acttgtacct gtaaaacaaa ggacagcatt gaggactgaa 300
acttgtctct tttttgaaca actgtgcaag aaaatatatc cctttttaaa aaacatcagt 360
tatggctaaa ctacaatcta gtgtctagaa ttacaaagaa taaaatgaaa tcaaagattt 420
ctcgctagta aaatgaaatg ttaggaacag tattaataa taggtcctac cccaacgaca 480
cttacacaga gcccgagtaca gtacctatta ttaacaggac gcatagctta aggaggaacc 540
acatcaaata ttcagccaga catatctagc ctcaagaagt caaaaaaaaa aaaaagcccc 600
aaacgaagac acccacactg agtaggggtg atgccgtgag tgctgtaatc aagattaaaa 660
agacctcagt ttttcttttt agactgttga tagtgacaat aaccattatg cttcccttaa 720
aagctctcaa ttcaatgtct gaaacatgaa tgttttcata tcaaaaagaa ctgatgtacc 780
tgccacccctc taaaaaagttt aagaattacc ctgcaaacat tgcactgatg aaggctgtca 840
cgacttacag agcctaagga ggacccaatg gcaggcatca gcacagctga acaccacctg 900
gaccccaactg cagccctgcc cagcgagctc tcacggagca gacacagtcc tcaagtaata 960
agcacagatg gaggagaaac gagaggctgt ggaaggcagg agagaaaagg cgagagacga 1020
gtttgttaaga atgccaaaagt caccttcccc attgtgggag gaaaatgccca aaggcactgg 1080
ttctgtgccc acaggcagtc tgagcacctg gagttgtgac gtccttccag gagagggtgc 1140
accaaggagc aggaggtttg tcaaagctct ggtcccacca acaagaacct cccaaagcaal 1200
agcagccccc attgaggttc caaggtcgtt ttgctgaaga cgggaacgaa accaacacca 1260
aagcgacagg ggggttgacag aggggacagg ggctgggcac cggcaacatg gagccgttca 1320
agtaaacata aaccacccaaa tacttagaaa aggcttgtaa acgagtgatc cgaaagggtc 1380
tctttgcagc atctctgatc agctggctaa agaaagggtg gtgctgaacc cgtcttagt 1440
gttatctgtt ttgtgttaaa gcacacgtgt gacacgggca gagtgtgtgg gcctgggct 1500
ggatcgcacg cagccgtggc cctctgtcta caaaggaggt gcttctgggt cctggttccg 1560
gatccttccc ccgcatgttc atagacggac agacttctac ttccagtcgc tagaaaagag 1620
ctgagtcctg tgctccctca ggcgccagc tgcagtcac caccagcacg cattctccta 1680
gagcgggcag gctggaatcc acaggacttt atttgttct tgattgacca ttgccaagat 1740
ctgagtgcaa atgcttgaca gggctcctcc ctggatgacc cctgcaaaaag agccccccag 1800
acacgtcatt cagctcagag taagacccca gggttgaggc aaggcagtac agcttgact 1860
ctttctactg tgtggctgtc tgctttgtgc tccttggcac tctgtccat cccacactga 1920
ctctcct

```

1927

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 672 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
gcctttttat tttttttttt tggtcgttat gctgcattta ttatgagaat caacagtcaa 60
cagttaatga ttgactaact cttgttggtc actctggaca ttaacgaaaa agactggaat120
agggtacag cgctgctttt atgctacacg ggttatgctt ggactctgac tcccagcagc180
aggtagattc aggaattcat ggcagtgaca ttcacatca tgggaaacac cttccctttt240
cttcaggatt ctctgtagtg gaagagagca cccagtgttg ggctgaaaac atctgaaagt300
agggagaaga acctaaaata atcagtatct cagagggctc taagggtgcc aagaagtctca360
ctggacattt aagtgccaac aaaggcatatc tttcggaatc gccaaagtcaa aactttctaa420
cttctgtctc tctcagagac aagtgaagct caagagtcta ctgctttagt ggcaactaca480
gaaaactggt gttacccaga aaaacaggag caattagaaa tggttccaat atttcaaagc540
tccgcaaaca ggatgtgctt tcccttgccc atttagggtt tcttctcttt cctttctctt600
tgtttagtct tcgttctctt tttcagtttc catcagatct cccctctgtg ccaactggaat660
ctcagagggt gc 672
```

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 269 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
ccgcataccta gccgcccgaact cacacaaggc aggtgggtga ggaaatccag agttgccatg 60
gagaaaaattc cagtgtcagc attcttgccg cttgtggcgc tctoctacaa tctggccagg120
gatagcacag tcaaacctgg agccaaaaag gacaggaagg agtctcgagc caaactgcgc180
cagaccctct ccagaagtgg gggtgaacaa ctcatctgga ctcagacgta tgaagaagct240
ctatataaat cgagactagc aactaacc 269
```

(2) INFORMATION ON SEQ ID NO. 31:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 604 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```
tgcgagggcg ggatagctgt ccaaggtctc ccccagcact gaggagctcg cctgctgccc 60
tcttgccgcg ggaagcagc accaagttca cggccaacgc cttggcacta gggccagaa120
tggtacaaac agtccctgat ggttgccgca atggcctgaa atccaagtac tacagacttt180
gtgataaggc tgaagcttgg ggcacgtcc tagaaacggg ggccacagcc ggggttgtga240
cctcggtggc cttcatgctc actctcccga tctctgtctg caaggtgcag gactccaaca300
ggcgaaaaat gctgcctact cagtttctct tctctctggg tgtgttggg atctttggcc360
tcaccttcgc cttcatcctc ggactggagc ggagcacagg gccacacgc ttcttctct420
ttgggatacct cttttccatc tgcttctcct gcctgctggc tcatgctgtc agtctgacca480
agctcgctccg ggggaggaag cccctttccc ggttggtgat tctgggtctg gccgtgggct540
tcagccctagt ccaggatggt atcgctattg aatatattgt cctgacgatg aataggacca600
aggt 604
```

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 781 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

```

ctttaatgtg cctagagcaa tggaatgggg cactttgggg gcggtggaat tcaagacgct 60
ctggctgaag attcagaagt atctggtaac tctcttttcc ttctgggcat cctctctctt120
gttctaatacc tcccttacac tcattcctgg tccattgtat tctgaccaca tcccttaatca180
tggtaaaaaa tattgagtcg tgggcacatt ggatcatgaag gaacaagaag gcaatgagag240
actctcatgc caaccactgc cctgaaagcc ctgctgttca gacagcaaag gggccagcac300
tggccaagct cttatgcttg ctctgaaacc ttcttgggag gagtcaatag ggtctccttt360
tgaaagtgtc cctggccttt tgagaaagca gtgtggtgga gggagatggg tctggcaggg420
gocgtgaatg gttgttttct acctgggatt tctttcctgc tttaggagat ctattgggaa480
actgattata accactcggg caccatcgat gcccacgaga tgaggacagc cctcagggaag540
gcagggttca cctcaacag ccagggtgcag cagaccattg ccctgcggta tgcgtgcagc600
aagcttggca tcaactttga cagcttcctg gcttgatga tccgcctgga gaccctcttc660
aaactattca gccttctgga cgaagacaag gatggcatgg ttcagctctc tctggccgag720
tggctgtgct gcgtgttggc ctgaccgcc aaacttgacc tagaagatgg ggggggcctc780
c

```

781

## (2) INFORMATION ON SEQ ID NO. 33:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
ggccactgcg gcgagacgcg aggaactgtc gctcgtactc gtgcgcctcg ctttgctttt 60
cctccgcaac catgtctgac aaacccgata tggctgagat cgagaaattc gataagtcga120
aactgaagaa gacagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac180
aggagaagca agcaggcgaa tcgtaaggag gcgtgcgcgc ccaagtatgc actgagatgc240
gagaagtgtt gcgtcgaatt tacctgcttg agggggtaaa gttgggaagg tggaaaagg300
gtgg                                     304
```

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1528 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
aattcggatc catgggccac agtggatggc ttgaaatgtg gctgagcgct tcggacactt 60
cggatccatg gtggccaccc caagacgcgc cccagcccgc catggcccgg atcctccggg 120
atcctgcctt ctgtccctgc tcttgccggg gtttgttccg ccgggcccgg gacaagagaa 180
gtctaagaca gactgccatg gcggtatgag tggtagcatc tacgagtatg gagccctcac 240
catcgatggg gaggaatata ttctttttaa gcagtatgca ggcaaatata tctcttttgt 300
caacgtagcc agctactgag gtctgacaga ccaatacctt gaactgaatg cactacaaga 360
agaacttggg ccatttggct tggtcattct gggttccct tccaaccaat ttggcaaaca 420
ggagccaggc gagaactcgg agatactccc cagtctcaag tatgttcgac caggtggggg 480
ctttgtgctt aatttccagc tctttgagaa aggagatgtg aacggggaga aagagcagaa 540
attctacact ttctgaaga actcctgccc tccactgca gaactcctgg gctcacctgg 600
ccgctctttt tgggaaccca tgaagatcca tgacatccgc tggaaacttg agaagttcct 660
ggtggggcca gatggcatac cggttatgcg ctggtaccac cggaccacag tcagcaacgt 720
caagatggac atcctgtctt acatgaggcg gcaggcagcc ctgagcgcca gggggaagta 780
actgatgccc ccaccctacc cctacccctt gccatcatg caagggccga ggaggggctc 840
ttcaggaagg aagccacatt cccagtcatt ctacccccac ccagattct ctttcttatt 900
acataaaaaga caagcctggc acaactgtgt gctcgaacca ctgtggacac gtgacaattg 960
```

```

tcccagtggtg  tgcattggota  cacagccacg  tatctgcctg  cttgaaaccc  agggatgggtc1020
catcttggtt  tacggcttgg  cacaacaccc  tcataatttt  ttcagctttc  tgttccaaat1080
gagcccaaaag  gaaaacacaag  ttctaggtcc  aatggttctg  ctcaaacctg  aacatcattc1140
ttgggggcaag  catctcccaac  atgcccacac  tacacaccac  cagcctcctt  cttccttctt1200
gaaggaccc  cctgagcccc  caagcccatc  ccacagtgtc  cctgagacca  gccaaagaca1260
ctgtgagcgc  gatggcctgt  taccccaggt  caggggtgtg  gtctctatga  aggaggggcl1320
cgaagccctt  gtgggcgggc  ctcccctgag  cccgtctgtg  gtgccagccc  ttagtgcat1380
caggcttagg  ctcccaggca  gggacactac  ccccgccct  ctggaggaca  tgctatctcl1440
tcactctgtc  cactggtatc  tcaacacccc  catctgccc  gtaaagggtc  ttctgcagca1500
aaaaaaaaaa  agaaaaaaaa  aaaaaaaaaa

```

1528

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 499 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

ggcagggtctc  agcgctcctc  cccctgctcc  gctcctctgc  agggcccagg  cgcccttggc 60
cttaggaccc  aacttctctt  accgccatgg  agttcgacct  gggagcagcc  ctggagccca120
cctcccagaa  gcccggtgtg  ggggcgggcc  acgggggaga  tcccagctc  agtcccaca180
aagttcagg  ccggtcggag  gcaggggcag  gtccgggtcc  aaagcaagga  caccacagct240
cttcgactc  cagcagcagc  tccagcgatt  cggacaagga  tgtgaagtcc  cacgtgctg300
gtcccaagca  gcacgagagc  atcccgggca  aggccaagaa  gcccaaagt  aagaagaagg360
agaagggcaa  gaaggagaag  ggcaagaaga  aggaggtccc  cactgaagg  gccctggaca420
gggctcatta  aaccttcctc  tctgcctacg  agtaccaccc  acctggagct  aagatgctta480
gggtggggggg  ggccgcccga

```

499

## (2) INFORMATION ON SEQ ID NO. 36:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gggcacccgt tagttgggaa cagcgggaacg ctgggtcccg ggactgagta aggtgtctgg 60
atcggagggga gggttcgggtg ggcatcgggc ggctggaaga gctcgactcg tcccgctggg 120
aaagcgcgag tctgagtggg accctggacg acttgacagag cggctggcgc agtcatggcg 180
gactactgga agtcacagcc aaagaaattc tgtgattact gcaagtgctg gatagcagac 240
aataggccta gtgttggaatt tcatgaaaga ggaaagaatc ataaggaaaa tgtggcaaaa 300
aggatcagtg agattaaaca gaaaagcctg gataaggcaa aggaagaaga aaaggcatca 360
aaggagtttg ctgcaatgga ggcagctgcc ctgaaagcat accaagagga tttgaaaaga 420
cttggccttag agtcagaaat tttggagcca agcataaacac cagtaaccag cactatccca 480
cctacctcga catcaaatca acagaaagaa aagaaagaga agaagaaaaa aagatccttc 540
aaagggcaga tgggtagaag gcataacctc tgagggttac cattactatt atgatcctat 600
ctcaggagca tctcagtggt agaaacctga aggatttcaa ggagacttaa aaaagacagc 660
agtgaagacc gtttggttag aagggttaag tgaagatggt tttacctatt actataatac 720
agaaacagga gaatccagat gggagaaaacc tgatgatttc attccacaca ctagtgatct 780
gccttctagt aagggtcaatg aaaattcact tggcacccta gatgaatcca aatcatcaga 840
ttcgcatagt gattctgatg gggaacagga agcagaagaa ggaggggtct ctacagagac 900
agaaaagcca aaaataaagt ttaaggaaaa aaataaaaaat agtgatggag gaagtgaccc 960
agaaacacag aaagaaaaaa gtattcagaa acagaattca ttaggttcaa atgaagaaaa1020
atcgaaaact cttaagaaat caaacccata tggagaatgg caagaaatta aacaagaggt1080
tgagtctcat gaggaggtag atttggaaact tocaagcact gaaaatgagt atgtatcaac1140
ttcagaagct gatggtggcg gagaacccaa agtgggtattt aaagaaaaaa cagtcacttc1200
tcttgagatt atggcagatg gagtggcccc agtcttcaaa aagagaagaa cttgaaaatg1260
ggaaaatctt aggaaaattt aagggcaacg aggtgatgat ccaatagttt gcagggagag1320
cttttttgtt acatgctttt tagggaccag aatggggaga ctttttgcca cccccaagt1380
ttgtcccgtg ttttgt                                     1396

```

## (2) INFORMATION ON SEQ ID NO. 38:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 808 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

cctctgtcca ctgctttcgt gaagacaaga tgaagttcac aattgtcttt gctggacttc 60
ttggagtctt tctagctcct gccctagcta actataatat caacgtcaat gatgacaaca120
acaatgctgg aagtgggcag cagtcagtga gtgtcaacaa tgaacacaat gtggccaatg180
ttgacaataa caacggatgg gactcctgga attccatctg ggattatgga aatggccttg240
ctgcaaccag actctttcaa aagaagacat gcattgtgca caaatgaac aaggaagtca300
tgccctccat tcaatccctt gatgcactgg tcaaggaaaa gaagcttcag ggtaaggga360
caggaggacc acctcccaag ggctgatgt actcagtcaa cccaaacaaa gtcgatgacc420
tgagcaagtt cggaaaaaac attgcaaaca tgtgtcgtgg gattccaaca tacatggctg480
aggagatgca agaggcaagc ctgttttttt actcaggaac gtgctacacg accagtgtac540
tatggattgt ggacatttcc ttctgtggag acacgggtgga gaactaaaca attttttaaa600
gccactatgg atttagtcat ctgaatatgc tgtgcagaaa aaatatgggc tccagtgggt660
tttaccatgt cattctgaaa tttttctcta ctagttatgt ttgatttctt taagtttcaa720
taaaatcatt tagcattgaa acggagaact ctgcgggcta gtaaccacaa ggtacggagc780
aaagatcacc cagggtggaa gaggtgga                                     808

```

## (2) INFORMATION ON SEQ ID NO. 39:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1139 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO



(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

```

tttttttttt tttttttttt ttttttgcag caatacctcc tttatttgat ccctgtttat 60
gtccacatat gtactgtatt atcacagatg caactgattt atcatagagc actcagaaaa 120
catggaaaag tattttttaa aatcgaataa tcctattcaa gtcaaccagt gtttaaccccg 180
gtgtgcttcc tgccagctctg ttcttcccca tgggagtcac acaaaatgaa aatctcctag 240
aaagagaaat tcctctgtcc tctgacttct tcaetttaga cgctgcgacc ttcccatggt 300
gttcaacatc ctcaactcgg agcgtcactg gctggagggtg gtctataaat ggaattggct 360

taactatctc ttcactgaaa ggtggacatt tagggagtgt ccagttttca gctgtcataa 420
acaactgcct tagacggcaa agaattcaca ggtcaatcgt tcccttcgct ttgaacttct 480
tcgcagaccg ttcacttgac cgaagctgga atttgctccc gtaaattgtag gaaataaagc 540
catcggtttc cacagtgaac acgcagttta gcttggggat aactttcagg cggtcttctt 600
tggtgataat tttgaaaatg tgctttgttt cctgtagaag gattcctgta ataccacat 660
aagaggggca tttggatttt gtcactgaaa taatagcccc gtgaagatct gcctttaaga 720
gcttggcctg aatcatctgt ggctgcgtgt ctggcttgag cccactgcac aggtccctga 780
tgtactgttt ccagagttca tggagaggga ggaaaaggct gtatctctgc tgcctgtggt 840
taatgtcaaa gagccgcagc tccctccttt gcctggcaga gaagcctttg gctttcttct 900
tcttctcctt gcgcttggtg cgggtgaagt actccaggac caccgccttg cgctgcagct 960
ggctcctcgc ggccctgcgg ctcatgcggg gcgtctgcgc ttcaggaagg cctcaccgaa1020
ggcctcggcc cgctgtgctc ctgaaggctg gacatcggag tcattcgctt ctttctgaga1080
caatgcatgg tagatcacac tcttcattct cggaccgctt ccggcgctct ctgatgacg 1139

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2177 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

```

gcccacgcgt cccgtcgcgc cccgcagcga acagcagcag cagtcagcct tcattcagga 60
aagacagcca gttgctctca tgcgtttatt gtctttcaat gtgcctcata ttaaaaacag 120
cacaggagaa ccaatatgga aggtactcat ttatgacaga tttggccaag atataatctc 180
tcctctgcta tctgtgaagg agctaagaga catgggaatc actctgcac tgcttttaca 240
ctctgatoga gatcctattc cagatgttcc tgcagtatac tttgtaatgc caactgaaga 300
aaatattgac agaattgtgc aggatcttcg aaatcaacta tatgaatcat attattttaa 360
ttttatttct gctatttcaa gaagtaaaact ggaagatatt gcaaatgcag cggttagcagc 420
tagtgcagta acacaagtag ccaaggtttt tgaccaatat ctcaatttta ttacttttga 480
agatgatatg tttgtattat gtaatcaaaa taaggagctt gtttcataac gtgccattaa 540
caggccagat atcacagaca cggaaatgga aactgttatg gacactatag ttgacagcct 600
cttctgcttt tttgttactc tgggtgctgt tcctataatc agatgttcaa gaggaacagc 660
agcagaaatg gtagcagtga aactagacaa gaaacttcga gaaaaatctaa gagatgcaag 720
aaacagtcct tttacaggtg atacacttgg agctggccaa ttcagcttcc agaggccctt 780
attagtcctt gttgacagaa acatagattt ggcaactcct ttacatcata cttggacata 840
tcaagcattg gtgcacgatg tactggattt ccatttaaac agggtttaatt tggagaatc 900
ttcaggagtg gaaaactctc cagctgggtg tagaccaaag agaaaaaaca agaagtctta 960
tgatttaact cccgttgata aattttggca aaaacataaa ggaagtccat tcccagaagt 1020
tgcagaatca gttcagcaag aactagaatc ttacagagca caggaagatg aggtcaaacg 1080

```

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acttaaaagc attatgggac tagaagggga agatgaagga gccataagta tgctttctga 1140
caataccgct aagctaacat cagctgttag ttctttgcca gaactccttg agaaaaaaag 1200
acttatggat ctccatacaa atgttgccac tgcctgttta gaaatataaa aggcaagaaa 1260
attggatgta tattttgaat atgaagaaaa aataatgagc aaaactactc tggataaaatc 1320
tcctctagat ataatatcag accctgatgc aggaactcca gaagataaaa tgagggtgtt 1380
tcctatctat tatataagca cacagcaagc acctctgag gctgatttgg agcaatataa 1440
aaaagcttta actgatgcag gatgcaacct taatccttta caatatatca aacagtggaa 1500
ggcttttacc aagatggcct cagctccggc cagctatggc agcactacca ctaaaacca 1560
gggtctttta tcacagagtc tgaatacagg atcacagttt gtgatggaag gagtgaaga 1620
cctgggtttt aaacagcaaa atctacctgt tactcgtatt ttggacaatc ttatggagat 1680
gaagtcaaac cccgaaactg atgactatag atattttgat cccaaaatgc tgcggggcaa 1740
tgacagctca gttcccagaa ataaaaatcc attccaagag gccattgttt ttgtgggtgg 1800
aggaggcaac tacattgaat atcagaatct tgttgactac ataaagggga aacaaggcaa 1860
acacatttta tatggctgca gtgagctttt taatgctaca cagttcataa aacagttgtc 1920
acaacttggc caaaagtaac acagaagaac cttactatga taatctactt ggaatgtgga 1980
taaatgtaaa aagaagaaaa gttagaagag caatatgttt ccttctctgt aacagtgctc 2040
taacagtgaa aatcagagtt atttgttaat ttttaaggaa attatatact taatargtat 2100
tgatttaaaag aaacatttca gaaataaaat ttcaacattg taaaaaaaat gtcggctacc 2160
tacacggata atatcgc

```

2177

## (2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 402 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

```

ggcgccaggcc ccagccagct caggctacac tatcccagga tcagcatggc cgtccgccag 60
tgggtaaatcg ccctggcctt ggctgcccctc cttgttggtg acaggggaagt gccagtggca120
gcaggaaagc tccctttctc aagaatgccc atctgtgaac acatggtaga gtctccaacc180
tggtcccaga tgtccaacct ggtctgcggc actgatgggc tcacatatac gaatgaatgc240
cagctctgct tggcccggat aaaaacccaaa caggacatcc agatcatgaa agatggcaaa300
tgctgatccc acaggagcac ctcaagccat gaagtgtcag ctggagaaca gtggtgggca360
tggagaggat atgacatgaa ataaaagatc cagcccaact ga                               402

```

## (2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1349 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

```

cttcttttgc catcccatTT ccttggcaCT gcaccatttc cccaattatt ggccaatccc 60
taggctttct gggttttaca atggttgcga ccacaatcag gctcatagat ggctccaatt 120
taaaaaaaaa ggtaatggtg atggataaaa taagcagatc aagggaagtg tgctatcata 180
aaataactgt agcttcaaca tcttgagtac cagtttctcg gcagatagta aacatccaat 240
cacaagggat ttttcctgaa ggggtgtaaag ctggtttgaa aattcttcag tcacagagca 300
gcctacacat gccaataga aactgacaga cactagatgt gcttggaaga ttaaactacta 360
cgtacagaaa cagcagttac taagctcctc agtagtttct tgtctttttt aagtttcgct 420
gaatcgacag tttgcacaac gtgctatatt ctgtgggtca aaaccaagta aatactgtgt 480
aaagtgggca gatttttcca gctaagatca agaaaaaaca aattttctga taaaacaggt 540
ttagagtcag aaacactctc taaagtgcaa aactgatggt ccacgatctc aaatagctaa 600
aactcctgca gaatggaagg gagagacgtg aaacagggaa ataaattaca gtcagtgtcta 660
gttaatttag gaaaagggaa aaataaacca aactcaagtc ggtaaagttt atcaaaatat 720
tcaatgatgt agctttcccc actctctgtc acacacgctt gctaacaagt atattaaatt 780
aaggccaaat ttaacctgaa tgcgtttttt tttttctttt tattaagatc tgagatagga 840
acggtcatac ttagtactga aaggcagaca ataaaaagg ccatagaaagg ggggggaaag 900
gtactgtcta ttgttcgagg gattcaacca gagataaaac ctatatacaa gcatgtgtgt 960
agctcgaaat aaaaaataaaa ggactatttc atgtcatgac tgcttggttg cttcctcttc1020
atatgcattc cctgtgccat tctgtacata ggatgaacca gaaccaaggc catacaaatg1080
accacaatat ttggcatcat caatatgac ttcaaagaac atttctctca ttttgaaaaa1140
ggccattcct gtgagcaatg aatcagatcc tgctgatgt tgtggtccta tccgttcag1200
ctctaactgt tctgccacct cctgtaatcc accttgaga tttttcctgt catttatgat1260
gtgaagtacc tcatgaagag ctgcaaaaat ctctaactgt tctgccacct cctgtaattg1320
cgagtcagtg attgacgaaa taatagtgc 1349

```

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3552 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

atttaattctt cattcttcta ctatccccc aaactaatttc aatatcaaac ctaattaaac 60
acatcaactt cccactgtac accaccacat caatcaaat ctccttcatt attagccctc 120
taccocctatt aatatttttc cacaataata tagaatatat aattacaacc tggcactgag 180
tcaccataaaa ttcaatagaa cttaaaaataa gcttcaaaac tgactttttc tctatcctgt 240
ttacatctgt agcccttttt gtcacatgat caattatata attctcttca tgatatatac 300
actcagaccc aaacatcaat cgattcatta aatatcttac actattcctg attaccatgc 360
ttatcctcac ctccagccaac aacatatttc aacttttcat tggctgagaa ggggtgggaa 420
ttatatcttt cctactaatt ggatgatgg acggacgaac agacgcaaat actgcagccc 480
tacaagcaat cctctataac cgcctcggag acatcggatt catttttagc atagtttgat 540
tttccctaaa cataaactca tgagaacttc aacagattat attctccaac aacaacgaca 600
atctaatttc acttataggc ctattaatcg cagctacagg aaaatcagca caatttggcc 660
tccacccatg actaccatca gcaatagaag gccctacacc agtttcagca ctactacact 720
caagtacaat agtagttgca ggaattttcc tactgggtccg attccacccc ctccagacta 780
ataataactt tattttaaca actatacttt gcctcggagc cctaaccaca ttatttacag 840
ctatttgtgc tctcacccaa aacgacatca aaaaaatcat tgcccttctc acatcaagcc 900
aactaggcct gataatagt acgctaggaa taaaccaacc acacctagca ttccctacac 960
tctgtaccca cgcattcttc aaagctatac tctttatatg ctctggctca atcattcata 1020
gcctggcaga cgaacaagac atccgaaaaa taggaaacat caaaaaatc ataccattcal 1080
catcatcatg cctagtaatc ggaagcctcg cctccacagg aataccattc ctaacagggt 1140
tctactcaaa agacctaat attgaagcaa ttaatacctg caacaccaac gcctgagccc 1200
tactaattac actaatcgcc acttctataa cagctatgta cagcatacga atcatttact 1260
tcgtaacaat aacaaaaccg cgttttcccc cctaatctc cattaacgaa aatgaccag 1320
acctcataaa cccaatcaaa cgcctagcat tcggaagcat ctttgcagga tttgtcatct 1380
catataatat tccaccaacc agcattccag tctccacaat accatgattt ttaaaaaacca 1440
cagccctaatt tatttcagta ttaggattcc taatcgcaat agaactaaac aacctaaacca 1500
taaaactatc aataaataaa gcaaatccat attcatcctt ctcaacttta ctggggtttt 1560
tcccatctat tattcaccgc attacaccca taaaatctct caacctaaag ctaaaaaacat 1620
ccctaactct cctagacttg atctgggttag aaaaaaccat cccaaaatcc acctcaactc 1680
ttcacacaaa cataaccact ttaacaacca accaaaaagg cttaattaaa ttgtacttta 1740
tatcattcct aattaacatc atcttaatta ttatcttata ctcaattaat ctcgagtaat 1800
ctcgataata ataaaaatc cgcgaaacaa agatcaccca gctactacca tcattcaagt 1860
agcacaaacta tatattgccc ctaccccaat cctccttcc aacataactc caacatcatc 1920
aacctcatac atcaaccaat ctcccaaac atcaagatta attactccaa cttcatcata 1980
ataattaagc acacaaatta aaaaaacctc tataatcacc cccaatacta aaaaacccaa 2040
aattaatcag ttagatcccc aagtctctgg atattcctca gtagctatag cagtcgtata 2100
tccaaacaca accaacatcc cccctaaata aattaaaaaa actattaaac ctaaaaacga 2160
tccaccaaac cctaaaacca ttaaaacaacc aacaaaacca ctaacaatta aacctaaacc 2220
tccataaata ggtgaaggct ttaatgctaa cccaagacaa ccaacaaaaa ataatgaact 2280
taaaacaaaa atataattat tcattatttc tacacagcat tcaactgcga ccaatgacat 2340
gaaaaatcat cgttgtaatt caactacaga aacaccattc ggatccatga aaaacacacc 2400
cattatttaa aattattaac cactcattca ttgacctacc tgccccatcc aacatttcat 2460
catgatgaaa ctttgggtcc cttctaggag tctgcctaata agtccaaatc attacaggtc 2520
ttttcttagc catacactac acatcagata caataacagc cttttcatca gtaacacaca 2580
tttgtcgaga cgtaaattac ggggtgactaa tccgatatat acacgcaaac ggagcctcaa 2640

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tatttttttat ttgcttatto cttcatgtcg gacgaggctt atattatgga tcatatacat2700
ttatagaaac ctgaaacatt ggagtacttc tactgtttgc agtcatagcc acagcattta2760
taggctacgt ccttccatga ggacaaatat cattctgagg tgccacagtt attacaaacc2820
tcctatcagc catcccatat attggaacaa ccttagtoga atgaatttga gggggcttct2880
cagtagacaa agccaccttg acccgattct tcgctttcca cttcatctta ccatttatta2940
tcgcgggccct agcaatogtt cactctctct tcctccacga aacaggatca aacaacccaa3000
caggattaaa ctcagatgca gataaaattc catttcaccc ctactatata atcaaagata3060
tcctaggtat cctaatacata ttcttaattc tcataaccct agtattattt ttcccagaca3120
tactaggaga cccagacaac tacataccag ctaatccact aaacacccca ccccatatta3180
aaccogaatg atatttctta ttgcatacg ccattctacg ctcaatcccc aataaaactag3240
gagggtgtcct agccttaatc ttatctatcc taatttttagc cctaataacct ttcttcata3300
cctcaaagca acgaagccta atattcogcc caatcacaca aattttgtac tgaatcctag3360
tagccaacct acttatctta acctgaattg gggggcaacc agtagaacac ccatttatta3420
tcattggcca actagcctcc atctcatact tctcaatcat cttaattctt ataccaatct3480
caggaattat cgaagacaaa atactaaaat tatatccata aaaaaaaaac acgatcggtt3540
gacatatagg gc
3552

```

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 601 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

tttttttttt tttttttttt tgcaattcaa atgaacgttt atttcttaaa cccacacaga 60
gtaagggcag agcttagaga tgcctggcac agcatttctc atccaggatc acttcctcgt120
tccttcttct ttgctgggag catcttagat ttatatcatt ttctacaaag acaatatcct180
gaatggcagt cgcaggttta tttcaaagtt ggagtcttct caggaagtag ggggagactgg240
attcccagct aatggaattt tcaactgtgat gtctgtgttc tcagtgaatt cttccagaaa300
gccggaggag actgtctcaa catcagtaga gaactcagaa ttctgtttgt ttgctggctgg360
cgtgaagtcc atgatctgct cagagtcagt gcttaaatca tcatctgtat aatcctctag420
aggagctttt gtccctctgt atgatccag ttggtcaaag actgagttta gtaggtcaat480
gattgaattc tgtagttctt tattgattga aactaattct gacaggggga aagccacagt540
cagaccacag aagacagtga tcaccaggac cttgaaaagc atcatgcttt agtaggggta600
a
601

```

(2) INFORMATION ON SEQ ID NO. 45:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2147 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```

agaaggggaa caaaaaaaaa aatatctgaa ttttgaaaa ccacaaagct acaacactga 60
ccctctcttt tttttgagac ggagttttgc tcttggtacc caggtggag tgcagtggcg 120
tgatcttggc tcaactgcaac ttccgtctcc cgggttcaag tgattctcct gcctcagcct 180
cccaagtagc tgggtttata ggtgcccgc accagaccgc gctaatttt tagttttagt 240
agagacgggg tttcaccacg ttggccaggc tggctttaa tgacctctt atttttaact 300
tggatactcg ctattctgcc aaaagacaat ttctagagta gttttgaatg ggttgatttc 360
ccccactccc acaaaactctg aagccagtgt ctagcttact aaaaaagag ttgtatataa 420
tatttaagat gctgagattt tcataggaaa gctgaatgct gctgtaaagt gctctttaag 480
tctttttttt ttttaatccc cttctaata atgaaactag ggggaatttc ggggacagag 540
atgggatttg ttgtatgata aactgtatgt agtttttagt ctttctgttt tgagaagcag 600
tgggtggggc atttttaaga tggctggcta ctcttgtttt cctcatgat aataaatttg 660
tcataactca gtaacatgaa cttgccccta gaggtagttg ttaataattt tgaaatatta 720
aggtcttggc aagcttctga tgattcacac ctgtactact gattattaag caggacagac 780
tgagctttct gttgcaaata ccttgaggga gaaagtaatt tctaaatata cagagaggta 840
acttgactat atatgttgca tctgtgctt cccttcatat taatatttga taaagatttt 900
aatttatgta aaacttctaa agcagaatca aagctcctct tggggaaatg gcaagctttt 960
aggataggca agaccctgta tgaatagtag caaagcatta ccgcattgta gagaacacac 1020
tcgattaaaa atgttaagct atctgaaaaa taaaatgtgc aagctctcag gatggcacaal 1080
aacaaagggt aatgcttctt ggggcacatt tcttagaggg cttgtctgag gtgtaaatat 1140
aatcgacttt tgtttgtgtt acatgacttc tgtgacttca ttgaaaatct gcacaattca 1200
gtttcagctc tggattactt cagttgacct ttgtgaagg ttttatctgt gtagaatggg 1260
tgtttgactt gttttagcct attaaatttt tattttcttt cactctgtat taaaagttaa 1320
acttactaaa agaaaagagg tttgtgttca cattaaatgg ttttggtttg gcttctttta 1380
gtcaggcttt ctgaacattg agatatcctg aacttagagc tcttcaatcc taagattttc 1440
atgaaaagcc tctcacttga acccaaacca gactactctt actgcctctt ttctaaatgt 1500
tcaggaaaag cattgccagt tcagtccttt caaaatgagg gagaaaacatt tgcctgcctt 1560
gtaataacaa gactcagtgc ttatttttta aactgcattt taaaaattgg atagtataat 1620
aacaataagg agtaagccac cttttatagg caccctgtag ttttatagtt cttaatctaa 1680
acattttata tttccttctt ttggaaaaaa cctacatgct acaagccacc atatgcacag 1740
actatacagt gagttgagtt ggctctccca cagtccttga ggtgaattac aaaagtcagg 1800
ccattatcat cctcctgagt tatttgaaat gatttttttt gtacattttg gctgcagtat 1860
tgggtggtaga atatactata atatggatca tctctacttc tgtatttatt tatttattac 1920
tagacctcaa ccacagctct ctttttcccc ttccacctct ctttgccctg aggatgtact 1980
gtatgtagtc atgcactttg tattaatata ttagaaatct acagatctgt tttgtacttt 2040

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ttataactgtt ggatacttat aatcaaaact tttactagggt tattgaataa atctagtctt 2100
actagaaaaat aaaaaaaaaa aaaaaaaaaa ctcaagacta gttctctt
2147

```

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 623 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

```

cccacgcgtc cccggaaaacg gcggcgggcg cgacaggacc gaggggcctt agttggtggg 60
caagtcgggg atcccagaaa gagaagcgtg acccggaagc ggaaacgggt gtccgtccca120
gctccggcct gccagtgagc ttctaccatc atggacctat tgttcgggcg ccggaagacg180
ccagaggagc tactgcgcca gaaccagagg gccctgaacc gtgccatgcg ggagctggac240
cgcgagcgac agaaactaga gacccaggag aagaaaatca ttgcagacat taagaagatg300
gccaagcaag gccagatgga tgctgttcgc atcatggcaa aagacttggt gcgcaccccg360
cgctatgtgc gcaagtgtgt attgatgcgg gccaacatcc aggtgtgtgc cctcaagatc420
cagacactca agtccaacaa ctgatggca caagccatga aggggtgtcac caaggccatg480
ggcaccatga acagacagct gaagttgccc cagatccaga agatcatgat ggagtttgag540
cggcaggcag agatcatgga tatgaaggag gagaggattg aattgttgca ttgatgatc600
ccgtgggttt tggggaagtt tta

```

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## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 781 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN



## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

```

gcggttatat tgcaagcttg aaaaactaaa agatctgtga aagatgctgc caagaagggc 60
cagaaggatg tctgcatagt tctggccaag gagatgatca ggtcaaggaa ggctgtgagc 120
aagctgtatg catccaaagc acacatgaac tcagtgtca tggggatgaa gaaccagctc 180
gcggtcttgc gagtggctgg ttccctgcag aagagcacag aagtgatgaa ggccatgcaa 240
agtcttgtga agattccaga gattcaggcc accatgaggg agttgtccaa agaaatgatg 300
aaggctggga tcatagagga gatgttagag gacacttttg aaagcatgga cgatcaggaa 360
gaaatggagg aagaagcaga aatggaaatt gacagaattc tctttgaaat tacagcaggg 420
gccttgggca aagcaccag taaagtgaat gatgcccttc cagagccaga acctccagga 480
gcgatggctg cctcagagga tgagggggag gaggaagagg ctctggaggc catgcagtcc 540
cggctggcca cactccgcag ctaggggctg cctacccgcg tgggtgtgca cacactcctc 600
tcaagagctg ccattttatg tgtctcttgc actacacctc tgttgtgagg actaccattt 660
tgagagaagg ttctgtttgtc tcttttcatt ctctgccag gttttgggat cgcaaaggga 720
ttgtctttat aaaagtggca taaataaatg catcattttt aggaaaaaaa aaaaaaaaaa 780
a

```

## (2) INFORMATION ON SEQ ID NO. 48:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1714 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

```

gttgcgacat gcagtgcgcc ggaggaactg tgctctttga ggccgacgct agggggcccg 60
aagggaaaact gcgaggcgaa ggtgaccggg gaccgagcat ttcagatctg ctccgtagac 120
ctggcgacc accaccatgt tggctgcaag gctggtgtgt ctccggacac taccttctag 180
ggttttccac ccagctttca ccaaggcctc cctgttgtg aagaattcca tcacgaagaa 240

tcaatggctg ttaacaccta gcagggaata tgccacaaaa acaagaattg ggatccggcg 300
tgggagaact ggccaagaac tcaaagaggc agcattggaa ccatcgatgg aaaaaatact 360
taaaattgat cagatgggaa gatggtttgt tgctggaggg gctgctgttg gtcttgagc 420
attgtgctac tatggcttgg gactgtctaa tgagattgga gctattgaaa aggctgtaat 480
ttggcctcag tatgtcaagg atagaattca ttccacctat atgtacttag caggagat 540
tggtttaaca gctttgtctg ccatagcaat cagcagaacg cctgttctca tgaacttcat 600
gatgagaggc tcttgggtga caattggtgt gacctttgca gccatggttg gagctggaat 660
gctggtacga tcaataccat atgaccagag cccaggccca aagcatcttg cttggttgct 720
acattctggt gtgatgggtg cagtgtgtgc tctctgaca atattagggg gtcctcttct 780
catcagagct gcatggtaca cagctggcat tgtggaggc ctctccactg tggccatgtg 840
tgcgccagct gaaaagtttc tgaacatggg tgcacccctg ggagtgggccc tgggtctcgt 900
ctttgtgtcc tcattgggat ctatgtttct tccacctacc accgtggctg gtgccactct 960
tactcagtg gcaatgtacg gtggattagt tcttttcagc atgttctctc tgtatgatac 1020
ccagaaagta atcaagcgtg cagaagatc accaatgtat ggagttcaaa aatatgatcc 1080
cattaactcg atgctgagta tctacatgga tacattaaat atatttatgc gagtgcacac 1140
tatgttgga actggaggca acagaaagaa atgaagtga tcagcttctg gcttctctgc 1200
tacatcaaat atcttgttta atggggcaga tatgcattaa atagtttgta caagcagctt 1260
tcgttgaaat ttagaagata agaaacatgt catcatatct aaatgttccg gtaatgtgat 1320
gcctcaggtc tgcccttttt tctggagaat aaatgcagta atcctctccc aaataagcac 1380
acacattttc aattctcatg tttgagtgat tttaaaatgt tttggtgaat gtgaaaacta 1440
aagtttgtgt catgagaatg taagtctttt ttctacttta aaatttagta ggttcactga 1500
gtaaactaaaa tttagcaaac ctgtgtttgc atattttttt ggagtgcaga atattgtaat 1560
taatgtcata agtgatttgg agcttttgta aagggaccag agagaaggag tcacctgcag 1620
tcttttgttt ttttaaatac ttaggaactt agcacctggg gttatttgga ttaggtgagg 1680
gagcccggtg ggaacagccc ggtattgggg aaca 1714

```

## (2) INFORMATION ON SEQ ID NO. 49:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 831 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

caccccagc ccctgctctg aggcaccgag aaacgaggag gcccggtggcg agtctccacg 60
tgggtaccgg cgctctcggc gcccgtagcc acccgcccgc cggaagccga catctcgagt120
tctggcagaa gcaatttgcg cggcgaggag cggacgggca ggaacccaat aagctgcttc180
gcctcggagc tgaagcccggt actcaagatg gcggctccgg gcgggcgtgg ccagtgacta240
gaaggcgagg cgccgcggga ccatggcggc ggccggcgac gagcgagtc cagaggacgg300
agaagacgag gaagaggagg agcagttggt tctggtggaa ttatcaggaa ttattgattc360

agaacttctc tcaaaatgtg aaaataaatg caaggttttg ggcattgaca ctgagaggcc420
cattctgcaa gtggacagct gtgtctttgc tggggagtat gaagacactc tagggacctg480
tggtatattt gaagaaaatg ttgaacatgc tgatacagaa ggcaataata aaacagtgtc540
aaaatatata tgccatacaa tgaagaagct cagcatgaca agaactctcc tgacagagaa600
gaaggaaagg gaagaaaaca taggtggggg ggaatggctg caaataaagg ataatgattt660
ctoctatcga cccaacatga tttgtaactt tctacatgaa aatgaagacg aagaagtgg720
agcttcagcc ccagataaat ctttgggaatt ggaagaggaa gagattcaaa tgaaccaccg780
gttcaaaccc ggggtttgtt aaaccgggga acccattgag ccttgggaat t      831

```

## (2) INFORMATION ON SEQ ID NO. 50:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 744 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```
tgaagttcta agagctttcc aagtttggga aggtgtccgg gttttctgcg attactttctc 60
tgagcatgaa cggaagtcac cctttgtgcc ttatgcgggtg attttaaatga taggtgtcat120
atataggacg gagtaatctg tttacattct gttcttctcg atgcactcac aagcgggtaa180
ctaggtgaca agaaaacaaa gatcttattc aaaagagggtc ttacagcaac ccaacgtctc240
atcttcccat agtaaagatg acggcgccctt gaggttaagct acaggcaaca ccacttccgc300
gtttctcttg cgccctggtc caagatggcg gatgaagcca cgcgacgtgt tgtgtctgag360
atcccgggtg tgaagactaa cgccggaccc cgagatcgtg agttgtgggt gcagcgactg420
aaggaggaa atcagtcctt tatccggtat gtggagaaca acaagaatgc tgacaacgat480
tggttccgac tggagtccaa caaggaagga actcgggtgg ttggaaaatg ctggtatatc540
catgacctcc tgaatatga gtttgacatc gagtttgaca ttcctatcac atatcctact600
actgccccag aaattgcagt tcttgagctg gatggaaaga cagcaaagat gtacaggta-
gactgaatag gagatggcaa agagtcaaag aaagccttaa ggaagaacct cgtggcgg
gggagagcat caggaagagt agct
```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2017 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

tgcgacccga ggcgcgcgagc aagatggcgg cgcgagtgcg ggcgcgcgcgc ggaggcgcgtg 60
ggcgcgcgcgc ctccctgcagc ggcgcgcgcgc ctgcagcctc ctgcccaggc tccggacatg 120
gacatcttcc agcaacagat ctcgagaaga cagctggcta aaatccttat ttgtccggaa 180
agttgatcca agaaaagatg ccactccaa tctcctagcc aaaaaggaaa caagcaatct 240
atacaaaatta cagtttcaca atgttaaacc ggaatgccta gaagcataca acaaaatttg 300
tcaagaggtg ttgcaaaaga ttacgaaga taaacactac ccttgractt tgggtggggac 360
ttggaacacg ttgtatggcg agcaggacca agctgtccac ctctggaggt atgaaggagg 420
ctatccagcc ctacagaag tcatgaataa actcagagaa aataaggaat ttttgaatt 480
tcgtaaggca agaagtgaca tgcttctctc caggaagaat cagctcctgt tggagttcag 540
tttctggaat gagcctgtgc caagatccgg acctaatata tatgaactca ggtcttacca 600
actccgacca ggaaccatga ttgaatgggg caattactgg gctcgtgcaa tccgcttcag 660
acaggatggt aacgaagccg tcggaggatt ctctctcag attgggcagc tctacatggt 720
gcaccatctt tgggcttaca gggatcttca gaccagggaa gacatacgga atgcagcatg 780
gcacaaacat ggctgggagg aattgggtata ttacacagtt ccacttattc aggaaatgga 840
atccagaatc atgatccac tgaagacctc gccctccag taaagctgta gatttctat 900
gtgcctacat acatttctgt gacaagtatt tgcgtaaat taattttaat tgtgtatcaa 960
gtgaaaaaga aacactgagg tttaagctg ctgtatatag cttgtgagaa acctcttttc 1020
tttaaaattt acataatcac aagaaaggaa agaattacag ttggactgat tgtgacagt 1080
ccttgtctgc ctctttgaaa ccccctgtg tgccagtat acctataac acctagccac 1140
ttctccccc cctccagaag ggtccacgt tgaattctga atcatcttga aaataagatt 1200
ccaaccacaa aaaaaattta gccatttctt tactaaaaaa aaccaaaaaa caaatctgtt 1260
ttataatcac agatttttag acaaatttct tgtatcagga agaaatacaa attttgtcat 1320
gtttctcaag cagtttttct gagtagtttc tgaggaggaa caaattacaa gtgtacccaal 1380
taactgaaaa tgttttaact cactctcatt tgtaagcagt ccacatagta gacaatgggt 1440
ttccaagct gggcaaggta catttaatca gtaaatcagt ttcacatcat gtattgtgat 1500
gtttcaatgt gagacacaaa aacaatggct tgaaacttgt gtatcatatg tgattttgaal 1560
atgaacacct tgaatagcac taatttttat ttgtggtatt tttctataac aaaacaagta 1620
gctctaggaa aagaggtttt attttgtaaa cgatcatttg tgacctcaga cactctctgg 1680
ctaataattt aataagctca cagcagataa ttctgagatc atgggtgagg ggtggtgcat 1740
gttgagattt aaattggcat aaagctgcat acttttgtc tagctgtttg atttcatttt 1800
ttaataragt atgccaattt tgtgactgtt acctgtgaa agtcctgttg aaatgaacaa 1860
ttgtctgccc cacaatcaag aatgtatgtg taaagtgtga ataaatctca tatcaaatgt 1920
caaaccttta catgtgaatg attttctcaa agaacataga aaagtcaata aaatcctctt 1980
aatttccaca aaaaaaaaaa aaaaaaaaaa aaaaaaa

```

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## (2) INFORMATION ON SEQ ID NO. 52:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 856 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

cgcagtgccg aggcgtgggg ctctctcctt gtcagtcggc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcggcgcc aggaactcgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgcc ttctccctgg agtaccgagt ctccctcaaa aatgagaaa gacaatatat180
atctccattt catgatattc caatttatgc agataaggat gtgtttcaca tggtagttga240
agtaccacgc tgggtctaag caaaaatgga gattgctaca aaggaccctt taaaccctat300
taaacaagat gtgaaaaaag gaaaacttcg ctatgttgcg aatttggtcc cgtataaagg360
atatacttgg aactatggtg ccatccctca gacttgggaa gaccagggc acaatgataa420
acatactggc tgttgtggtg acaatgacct aattgatgtg tgtgaaattg gaagcaagg480
atgtgcaaga ggtgaaataa ttggcgtgaa agttctaggc atattggcta tgattgacga540
aggggaaacc gactggaaag tcattgccat taatgtggat gatcctgatg cagccaatta600
taatgatata aatgatgtca aacggctgaa acctgggtac ttagaagcta ctgtggactg660
gtttagaagg tataaggttc ctgatggaaa accagaaaat gagtttgctt ttaatgcaga720
atttaaagat aaggactttg ccattgatat tattaaaagc actcatgacc attggaaaagc780
attagtgact aagaaaacga atgggaaaag gatcatgttg attgttcaac ttttcgttgg840
gccccctcaa gtgtgc                                     856

```

## (2) INFORMATION ON SEQ ID NO. 53:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 540 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```
gcatagacaa agggcctcag aatcgcgag ggcgaattgt gccctgggtc gccaaagatgt 60
cgttcccaaa gtataagcgg tcgagcctgc gcaactctgcc tgagaccctc gaccagccg120
aatacaacat atctccggaa acccggcggg cgcaagcgag cgggtggcca taagagccca180
gctgaaacga gactacctgc ttcagtacaa cgatcccaac cgccgagggc tcatcgaaaa240
tcctgccttg cttcgttggg cctatgcaag aacaataaat gtctatccta atttcagacc300
cactcctaaa aactcactca tgggagctct gtgtggattt gggccctca tcttcattta360
ttatattatc aaaaactgaga gggataggaa agaaaaaactt atccaggaag gaaaattgga420
tcgaacattt cacctctcat attaatctg gcaatgatga ctatatgtat tcctgcctaa480
ataaatcatc tattaatcat taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaagtcg540
```

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1912 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

tgtgtgagggc ccaacagcgg aatcatcgat gcagggggcct gaattaatgt atctgtgatg 60
ttacagcctt tcgattatga tcccaatgag aaaagttaaac acaggttatg gttcagtgcta 120
tggtttgctcc aactgacact tcagatatgg aagcagtatg gaaggaggca aaaccggaag 180
accttatgga ttcaaaaactt agatgtgtgt ttgaattgcc agcagagaat gataaaccac 240
atgatgtaga aataaataaa attatatcca caactgcata aaagacagaa acaccaatag 300
tgtctaagtc tctgagttct tctttggatg acaccgaagt taagaaggtt atggaagaat 360
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag ttcaagggaag 420
aagatggact gcggatgagg aagacagtgc agagcaacag cccatttca gcattagccc 480
caactgggaa ggaagaaggc cttagcaccg ggctcttggc tctggtgggt ttgttcttta 540
tcgttggtgt aattattggg aagattgcct tgtagaggta gcattgcacag gatggtaaat 600
tggattgggt gatccacat atcatgggat ttaaatttat cataaccatg tgtaaaaaa 660
aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttaccctcc ctgcacacac 720
atacacagat acacacacac aaatataatg taacgatctt ttagaaagtt aaaaatgtat 780

agtaactgat tgagggggaa aagaatgata tttattaatg acaagggaaa ccattgagtaa 840
tgccacaatg gcatattgta aatgtcattt taaacattgg taggccttgg tacatgatgc 900
tggattacct ctcttaaaat gacacccttc ctgcctgtt ggtgctggcc cttggggagc 960
tggagccag catgctgggg agtgccgtca gctccacaca gtagtcccca cgtggcccac 1020
tcccggccca ggctgcttcc cgtgtcttca gttctgtcca agccatcagc tcttgggac 1080
tgatgaacag agtcagaagc ccaaaggaaat tgcaactgtg cagcatcaga cgtactcgtc 1140
ataagtgaag ggcgtgtgtt gactgattga cccagcgctt tggaaataaa tggcagtgct 1200
ttgttcactt aaagggacca agctaaattt gtattggttc atgtagtga gtcaaaactg 1260
tattcagaga tgtttaatgc atatttaact tatttaatgt attcatctc atgtttctc 1320
attgtcacia gagtacagtt aatgctgcgt gctgctgaac tctgttgggt gaactggat 1380
tgctgctgga ggcgtgtggg ctctctgtc tctggagagt ctggtcatgt ggaggtggg 1440
tttatggga tgctgggaaa gagctgccag gaagtgtttt ttctgggtca gtaaaataca 1500
actgtcatag ggagggaaat tctcagtagt gacagtcaac tctaggttac ctttttaata 1560
gaagagtagt cagtcttcta gattgttctt ataccacctc tcaaccatta ctcacactc 1620
cagcgcacag gtccaagtct gagcctgacc tccccttggg gacctagcct ggagtcagg 1680
caaattggatc ggcgtgcaga gggttagaag cgagggcacc agcagttgtg ggtggggagc 1740
aaggggaagag agaaaactct cagcgaatcc ttctagtact agttgagagt ttgactgtga 1800
atataattta tgccataaaa gaccaaccca gttctgtttg actatgtagc atcttgaaaa 1860
gaaaaaattat aataaaagccc caaaattaag aaaaaaaaaa aaaaaatact gc 1912

```

## (2) INFORMATION ON SEQ ID NO. 55:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN



## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

tttttttttt ttttatcgag caagaatctg ttaacagttt tatttttttt tatgttaaat 60
accatgggac aggattgtaa ggatgaaaaa ctcaagtcaac aactgcctca caagggataa 120
gaaaaattct gccatgatat tagcaaagggt aaaggaggaa aaatttacac tgaagaggc 180
accatttccc caaggaatac ctcttgccat ttcttgaatg agtgggatta gcaatctaaa 240
taaatcatat ttcaagagggt aacagcaaca gataaaattt aaagggatta ttaaaataac 300
atttacaaga ctctgaacaa ttcttgaact cttattaaaa ccacaaagaa agaacaattc 360
tttatttatg aatttcataa aggactcaat gtgcaactga catctgctag tgatgatctg 420
gtaatataca acctgtccag tagccgaaca gtttggtttt attgtgtttt ctaaccgtaa 480
gagatcatta aaggcaaagc ctatatgacg ctgtacacac aaaaaaatgg tcaccgtggg 540
ccatactacc aatgaaatgg taggtaaaaca aatctttttc tgggtcaagag aaaaaaaaaa 600
aaaagaaaca gcactctgca tgcttcactc tacaagatga atttccctag aaagaatcca 660

atgaaaaatgg ctgcaattac aacaagaagt gaaggaagag gactgggtgac attatctctg 720
aaggatgcag ttgaggttga tccagggtta tccgaatgtg ctacctttct gagccttaaa 780
ccttcacctc tcagggtgcg attttcttct gatagcttca tcatttctcc ctgaagtctt 840
ttacactctt ccattagttt ccttggttct gtatcattaa gtgaaacact gtgtgggttt 900
ggcataggtc catcttgctt agatgcattc agtggaaacag ct-tgctagg ttccatatca 960
ttcaatttat cattttcatt gggcatttca aatacgcatc tcaatttgga atccattaat 1020
tcacacaggt ttgctctctt ccacacagct tccatatctg aagtgtttgg tggagcaaaa 1080
attgtctgta ccataaaact gtgtttactc ttttcattcg gatcatagtc aaagggctgt 1140
agcattactg aaacagtcac agttgacctt gggtaataa ttccactgtt gggcctcaca 1200
cagtaccggc gaggtgctgt agtcttcact ttgaaacaca cttttctatc cgatggattt 1260
cgcaatttaa gattttagt gactacatct gtgaaggggc ctttgaattt gaggtctgtg 1320
ggcgatcgca ggaccaggat ctgctcgtct tcgccatggc ccttgaggcg gacgccatcg 1380
gagagacagc gcagagcagg gggcggttct ctgctgggg gcgggggacg atggcgagag 1440
gggaggggga gcgagttcgc atctctcctt ttcttggtta gactctgttc aaccacattc 1500
ttatgttggc agatctgctt ccagattgat ttttagagca ccacactttt cacattcctg 1560
attctgattt tgttttgttt tgtttgggtt ttctgaaact taaaaatgctg cccccaaaat 1620
actatatttt tgagtttgtg ttctgaaaagc ctccgtgctg ctggatcttt ggggggaaaat 1680
acaggatcct tcagcactga ggtgtttaag atttgcaact agcaatgcaa tttttctaa 1740
atatggggat atttaccttt attaagaaat tatactaaac attgatgtcc ttgatcattt 1800
tatgtcttca tattactttt gattctacta tgattgtgtg gtggtgaaca aagatcatta 1860
caaacaaaaa ctgtaatttt gttatatttg attcaatgga atttacctaa aaaataaaga 1920
ctaaaaatgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa
1962

```

## (2) INFORMATION ON SEQ ID NO. 56:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

eggctcgagc ggctcgagat tcgaggctcgt ggtggtcttg gaagagcgtc gagggggccg 60
tggacgtgga atgggcccag gagatggatt tgattctcgt ggcaaacgtg aatttgatag 120
gcatagtgga agtgatagat ctggcctgaa gcacgaggac aaacgtggag gtagcggatc 180
tcacaactgg ggaactgtca aagacgaatt aacagagtcc cccaaatata ttcagaaaca 240
aatatcttat aattacagtg acttggtatca atcaaagtgt actgaggaaa cacctgaagg 300
tgaagaacat catccagtgg cagacactga aaataaggag aatgaagttg aagaggtaaa 360
agaggagggt ccaaaaagaga tgactttgga tgagtggag gctattcaaa ataaggaccg 420
ggcaaaagta gaattttaata tccgaaaacc aaatgaaggt gctgatgggc agtggagaag 480

gggatttggt cttcataaat caaagagtga agaggctcat gctgaagatt cggttatgga 540
ccatcatttc cggaagccag caaatgatat aacgtctcag ctggagatca attttgaga 600
ccttgccgcg ccaggacgtg gcggcagggg aggacgaggt ggacgtgggc gtggtgggcg 660
cccaaacctg ggcagcagga ccgacaagtc aagtgtctct gctcctgatg tggatgacct 720
agaggcattc ccagctctgg cttaactgga tgcataaga caacctgggt tctttgtga 780
acccttctgt tcaaagcttt tgcattgctta aggattccaa acgactaaga aattaaaaaa 840
aaaaagactg tcattcatac cattcacacc taaagactga attttatctg ttttaaaaaa 900
gaacttctcc cgctacacag aagtaacaaa tatggtagtc agttttgtat ttgaaaatgt 960
attggttagc gggatgtttt cataattttc agagattatg cattcttcat gaatactttt 1020
gtattgctgc ttgcaaatat gcatttccaa acttgaaata taggtgtgaa cagtgtgtac 1080
cagttttaaag ctttcaactc atttctgttt ttaattaag gatttagaag ttccccaat 1140
tacaaaactg ttttaaatat tggacatact ggttttaata cctgctttgc atattcacac 1200
atggtcaact gggacatggt aaactttgat ttgtcaaatt ttatgctgtg tggaaatact 1260
actatatgta ttttaactta gttttaatat ttctattttt ggggaaaaat cttttttcac 1320
ttctcatgat agctgttata tatatatgct aaatctttat atacagaaat atcagtactt 1380
gaacaaattc aaaagcacat ttggtttatt aaccctgggc tgccttgga tggggcccat 1440
ttgggggtcca aattataa
1458

```

## (2) INFORMATION ON SEQ ID NO. 57:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2188 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```

gggccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 120
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 180
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 240
ccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 300
ccaaccctcc cccacccccc cccctacaag tcacctggtt aagccaacct gaattctact 360
cacctgggag tggaagtatg tatgacagaa tgcgacgagg aggtgatgga tatgatggtg 420
gttatggagg ttttgatgac tatggtggct ataataatta cggctatggg aatgatggct 480
ttgatgacag aatgagagat ggaagaggta tgggaggaca tggctatggt ggagctggtg 540
atgcaagtgc aggttttcat ggtggtcatt tegtacatat gagagggttg ccttttcgtg 600
caactgaaaa tgacattgct aatttcttct caccactaaa tccaatacga gttcatattg 660
atattggagc tgatggcaga gccacaggag aagcagatgt agagtttggt acacatgaag 720
atgcagtagc tgccatgtct aaagataaaa ataacatgca acatcgatat attgaactct 780
tcttgaattc tactcctgga ggcggtctg gcattggagg ttctggaatg ggaggctacg 840

gaagagatgg aatggataat caggagggct atggatcagt tggaagaatg ggaatgggga 900
acaattacag tggaggatat ggtactcctg atggtttggg tggttatggc cgtgggtggtg 960
gaggcagtg aggttactat gggcaaggcg gcattgagtg aggtggatgg cgtgggatgt 1020
actgaaagca aaaacaccaa catacaagtc ttgacaacag catctggtct actagacttt 1080
cttacagatt taatttcttt tgtattttta gaactttata atgactgaag gaatgtgttt 1140
tcaaaaatatt atttggtaaa gcaacagatt gtgatgggaa aatgttttct gtaggtttat 1200
ttgttgcata ctttgactta aaaataaatt tttatattca aacctgatgt gttgataact 1260
tttatatact agttactcct aaagatgtgc tgccttcata agatttgggt tgatgtattt 1320
tactattagt tctacaagaa gtagtgtggt gtaattttag aggataatgg ttcacctctg 1380
cgtaaaactgc aagtcttaag cagacatctg gaatagagct tgacaaataa ttagtgtaac 1440
ttttttcttt agttcctcct ggacaacact gtaaatataa agcctaaaga tgaagtggct 1500
tcaggagtat aaattcagct aattatttct atattattat ttttcaaagt tcatttatca 1560
ggcatagctc tgaacattg atgatctaag aggtattgat ttctgaatat tcataattgt 1620
gttacctggg tatgagagt ttggaagctg aattctagcc ctagattttg gagtaaaacc 1680
ccttcagcac ttgaccgaaa taccaaaaat gtctccaaaa aattgatagt tgcaggttat 1740
cgcaagatgt cttagagtag ggttaagggt ctcagtgaac caagaattca gtattaagta 1800
cataggtatt tactatggag tataattctc acaattgtat tttcagtttt ctgcccataa 1860
gagtttaaat aactgtataa atgatgactt taaaaaaatg taagcaacaa gtccatgtca 1920
tagtcaataa aaacaatcct gcagttgggt tttgtatctg atccctgctt ggagttttag 1980
tttaaagaat ctatatgtag caaggaaaag gtgcttttta attttaatcc ctttgatcaa 2040
tatggctctt ttccaaattg gctaattgat caaaatgaaa cctgttgatg tgaattcagt 2100
tattgaactt gttacttgtt tttgccagaa atgttattaa taaatgtcaa tgtgggagat 2160
aaaaaaaaa aaaaaaaaaa aaaaaaaa

```

2188

## (2) INFORMATION ON SEQ ID NO. 58:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

ctcgctagtt cgatcggtag cgggagcgga gagcggaacc cagagagccc tgagcagccc 60
caccgccgcc gccggcctag ttaccatcac accccgggag gggccgcagc tgccgcagcc 120
ggccccagtc accatcacgc caaccatgag cagcgaggcc gagaccagc agccgccgcg 180
ggcccccccc gccggccccg cctcagcgc cgccgacacc aagcccggca ctacgggcag 240
cgggcgaggg agcgggtggc cgggcggcct caccatcggc gcgcctgccg gcggggacaa 300
gaaggtcatc gcaacgaagg ttttggaac agtaaaatgg ttcaatgtaa ggaacggata 360
tggtttcatc aacaggaatg acaccaagga agatgtattt gtacaccaga ctgccataaa 420

gaagaataac cccaggaagt accttcgcag tgtaggagat ggagagactg tggagtttga 480
tgtgtttgaa ggagaaaaag gtgoggaggc agcaaatgtt acagggtcctg gtgtgtttcc 540
agttcaaggc agtaaatatg cagcagaccg taaccattat agacgctatc cacgtcgtag 600
gggtcctcca cgcaattacc agcaaaatta ccagaatagt gagagtgggg aaaaagaacga 660
gggatcggag agtgctcccg aaggccaggc ccaacaacgc cgccctacc gcaggcgaag 720
gttccacact tactacatgc ggagacccta tgggcgtcga ccacagtatt ccaaccctcc 780
tgtgcaggga gaagtgtatg aggggtgctga caaccagggt gcaggagaac aaggtagacc 840
agtgaggcag aatatgtatc ggggatatag accacgattc cgcaggggcc ctccctcgcca 900
aagacagcct agagaggacg gcaatgaaga agataaaaga aatcaaggag atgagacca 960
aggtcagcag ccacctcaac gtcggtaccg ccgcaacttc aattaccgac gcagacgccc 1020
agaaaacccct aaaccacaag atggcaaaga gacaaaagca gccgatccac cagctgagaa 1080
ttcgtccgct cccgaggctg agcagggcgg ggctgagtaa atgccggctt accatctcta 1140
ccatcatccg gtttagtcat ccaacaagaa gaaatatgaa attccagcaa taagaaatga 1200
acaaaagatt ggagctgaag acctaaagt cttgcttttt gcccgttgac cagataaata 1260
gaactatctg cattatctat gcagcatggg gtttttatta tttttacctt aagacgtctc 1320
tttttggtaa taacaaacgt gtttttttaa aaagcctggt tttttctaat acgcttttaa 1380
aggtttttta attgtttcat atctggtcaa gttgagattt ttaagaactt cattttta 1440
ttgtaataaa agttttacaac ttgatttttt caaaaaagtc aacaaaactgc aagcacctgt 1500
taataaaggc cttaataaat tgtctttgtg taaaaaaaaa gggaatat 1548

```

## (2) INFORMATION ON SEQ ID NO. 59:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1254 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ggaccgcttc ccccgagcca gcagcagcgt ttgacgtcat cgtgcgtgtg gtgcccctgc 60
tgccggggct ggtgattgga ggaaaccccg tgtctgacgg agggctgtag cctgtgagca 120
gcgagatcca gggacagagt ctacgcctcg ccgctgctgc cgccgccgcc gccagagac 180
tgctgagccc gtccgtccgc cgccaccacc cactccggac acagaacatc cagtcattga 240
taaaaatgag ctggttcaga aggccaaact ggccgagcag gctgagcgat atgatgacat 300
ggcagcctgc atgaagtctg taactgagca aggagctgaa ttatccaatg aggagaggaa 360
tcttctctca gttgcttata aaaaattgtt aggagcccg aggtcatctt ggagggctcg 420
ctcaagtatt gaacaaaaga cggaagggtg tgagaaaaaa cagcagatgg ctcgagaata 480
cagagagaaa attgagacgg agctaagaga tatctgcaat gatgtactgt ctcttttggg 540
aaagttcttg atccccaatg cttcacaagc agagagccaa agtcttctat ttgaaaatga 600
aaggagatta ctaccgttac ttggctgagg ttgccgctgg tgatgacaag aaagggattg 660
tcgatcagtc acaacaagca taccaagaag cttttgaaat cagcaaaaag gaaatgcaac 720

caacacatcc tatcagactg gggctggccc ttaacttctc tgggttctat tatgagattc 780
tgaactcccg cagagaaaagc ctgctctctt gcaaagacag cttttgatga agccattgct 840
gaacttgata cattaagtga agagtctatc aaagacagca cgctaataat gcaattactg 900
agagacaact tgacattgtg gacatcggat acccaaggag acgaagctga agcaggagaa 960
ggaggggaaa attaacgggc cttccaactt ttgtctgcct cattctaaaa ttacacagtl1020
agaccatttg tcatccatgc tgtccacaa atagtttttt gtttacgatt tatgacaggt1080
ttatgttact tctatttgaa tttctatatt ttccctgttg gttttatgtt tagttttggg1140
ggagtaggag ccagtttaac gtttgaggag tttgtctgtt tttcgtcttt gaggggggcl200
ccagtatggg ggggtgttgg gattttttgt taccagtttt tgaggtgttt ttgg 1254

```

## (2) INFORMATION ON SEQ ID NO. 63:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 954 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```
cctctctctt ttctttttct tctttttttt ttctttttt ttttttgta gagcagggtc 60
actttattgg tatagagact gcagagggac caggggcttt agctgttggc agctatgggt120
tccttaatcc agtccacata gttgtagacc ttgggtgtaga ctccaggcct gttcttctgg180
gcacagccat agccccagga gacaattcct tggagctctc cattggagac cacagggccca240
ccagaatcac cctggcagga atccttgccct cctcagagga agccccacaca gaacatgttg300
ttggtaatct ttccagggtg ggaggcttca cactcagcct ggctcagcac aggagcatcc360
aggcactgca gctcgtctgg gtagtcggca ccagaactca gagtgttgcc ccagccggag420
atgagggact cgggtccagc agctggaggg gcagtgggca gagagatggc ggacacgcgg480
gaattgatga cggcaggtga ggagagcttg atcagcagga tgtcattgtc cagagtccgg540
ctgttgatt tgggggtggcg gatgatcttg gccgcattga tgaactgttc attccccctcc600
aggacttcga tgttggtgctc tcccagtctc acctggatgc gggacttgta gcagtgacct660
gctgacacca cccactgttc gctgatgagg gagccaccgc agaagtggta gccagaattc720
aaggacacct ggtaggggac agaattctcc tcacagatgt agcccccaac gatcttgta780
tcatcatcaa agggggcagc aacagcagct gcaacaaagg taaggatcag aagtagattc840
atgggtgtag agtgtgcctg attgctgggtg gagaaccctt ctttatacct cccgaggatg900
gggagaggag gtgtctgtga ggtgagggtc actgctcctc ccagcacaaa caca 954
```

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2213 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

```

ggcggaccgc cggggggtcg aggcctgcct ctccgagagc tcttggcgcg gccgtcccgg 60
ccccggggccc caggtgcgct tcccctagag agggattttc cgttctcgtg ggcagaggaa 120
caaccaggaa cttgggggtc agtctccacc ccacagtggg gcggtaccgt cccggataag 180
acccgctgtc tggccctgag tagggtgtga cctccgcagc cgagaggag gagcgagcc 240
ggcctcgaag aacttctgct tgggtggctg aactctgac ttgacctaga gtcattggcca 300
tggcaaccaa aggaggtact gtcaaagctg cttcaggatt caatgccatg gaagatgccc 360
agaccctgag gaaggccatg aaagggtctg gcaccgatga agacgccatt attagcgtcc 420
ttgcctaccg caacaccgcc cagcgccagg agatcaggac agcctacaag agcaccatcg 480
gcagggactt gatagacgac ctgaagtcag aactgagtgg caacttcgag caggtgattg 540
tggggatgat gacgcccacg gtgctgtatg acgtgcaaga gctgcgaagg gccatgaagg 600
gagccggcac tgatgagggc tgcctaattg agatcctggc ctcccgacc cctgaggaga 660
tccggcgcat aagccaaacc taccagcagc aatatggacg gagccttgaa gatgacattc 720
gctctgacac atcgttcatg ttccagcgag tgctggtgtc tctgtcagct ggtgggaggg 780
atgaaggaaa ttatctggac gatgctctcg tgagacagga tggccaggac ctgtatgagg 840
ctggagagaa gaaatggggg acagatgagg tgaaatttct aactgttctc tgttcccga 900
accgaaatca cctgttgcat gtgtttgatg aatacaaaaag gatatacag aaggatattg 960
aacagagtat taaatctgaa acatctggta gctttgaaga tgctctgctg gctatagtaa1020
agtgcattag gaacaaatct gcatattttg ctgaaaagct ctataaatcg atgaagggt1080
tgggcaccga tgataacacc ctcatcagag tgatgggttc tcgagcagaa attgacatgt1140
tggatatccg ggcaacttc aagagactct atggaaagtc tctgtactcg ttcataagg1200
gtgacacatc tggagactac aggaagtac tgcttgttct ctgtggagga gatgattaaal260
ataaaaaatcc cagaaggaca ggaggattct caacactttg aattttttta acttcatttt1320
tctacactgc tattatcatt atctcagaat gcttatttcc aattaaaacg cctacagctgl380
cctcctagaa tatagactgt ctgtattatt attcacctat aattagtcatt tatgatgctt1440
taaagctgta cttgcatttc aaagcttata agatataaat ggagatttta aagtagaaat1500
aaatatgtat tccatgtttt taaaagatta ctttctactt tgtgtttcac agacattgaal560
tatattaaat tattccatat tttcttttca gtgaaaaatt ttttaaattg aagactgttc1620
taaaatcact tttttcccta atccaatttt tagagtggct agtagtttct tcatttgaaal680
ttgtaagcat ccggtcagta agaatgcccc tccagttttc tatatttcat agtcaaagcc1740
ttgaaagcat ctacaaatct ctttttttag gttttgtcca tagcatcagt tgatccttac1800
taagtttttc atgggagact tccctcatca catcttatgt tgaatcact ttctgtagtc1860
aaagtatacc aaaaccaatt tatctgaact aaattctaaa gtatggttat acaaaccata1920
tacatctggt taccaaacat aaatgctgaa cattccatat tattatagtt aatgtcttaa1980
tccagcttgc aagtgaatgg aaaaaaaaaa aagcttcaaa ctaggatttc tgggaatgat2040
gtaatgctct gaatttagta tgatataaag aaaacttttt tgtgctaaaa atacttttta2100
aaatcaattt tgttgattgt agtaatttct atttgactg tgcctttcaa ctccagaaac2160
attctgaaga tgtacttgga ttaattaaa aagttcactt tgtaaaaaaa aaa 2213

```

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2878 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

```

cctcgtgcag gtgcacccgt tggtcctaaa agctctggag gatggccggg catatgggtc 60
tccatgggtgc aacaaacaga tcacaagggt cctaattgaa tgcgagatg aatataaata 120
taatgtggag gctgtggagc tgctaattcg caatcatttg gttaatatgc agcagtatga 180
tcttcaccta gcgcagtcac tggagaatgg cttaaaactac atggctgtgg catttgctat 240
gcagttagta aaaatcctgc tgggtggatga aaggagtgtt gctcatgta ctgaggcaga 300
tctgttccac accattgaaa cctcatgag gattaatgct cattccagag gcaatgctcc 360
agaaggattg cccagctga tggagtagt gcgatccaac tatgaagcaa tgattgatcg 420
tgctcatgga ggcccaaaact ttatgatgca ttctgggac tctcaagcct cagagtatga 480
tgacctcca ggctgaggg agaaggcaga gtatcttctg agggaaatggg tgaatctcta 540
ccattcagca gcagctggcc gcgacagtac caaagcttct tctgcatttg ttggacagat 600
gcaccagcaa ggaatactga agaccgatga tctcataaca aggttcttct gtctgtgtac 660
tgaaatgtgt gttgaaatca gttaccgtgc tcaggctgag cagcagcaca atcctgctgc 720
caatccacc atgatccgag ccaagtgtca tcacaacctg gatgccttg ttcgactcat 780
tgactgtctc gtgaaacact caggggaggg caccaacact gtcacaaaga ttaatctgct 840
gaacaaggtc cttggtatag tagtgggagt tctccttcag gatcatgat ttcgtcagag 900
tgaatttcag caacttccct accatcgaat ttttatcatg cttctcttgg aactcaatgc 960
acctgagcat gtgttggaaa ccattaattt ccagacactt acagcttctt gcaatacatt1020
ccacatcttg aggcctacca aagctcctgg ctttgtatat gcctggcttg aactgatttcl080
ccatcgata tttattgcaa gaatgctggc acatacgcca cagcagaagg ggtggcctat1140
gtatgcacag ctactgattg atttattcaa atatttagcg cctttcctta gaaatgtgga1200
actcaccaaa cctatgcaaa tctctacaa gggcacttta agagtgtgc tggttctttt1260
gcatgatttc ccagagttcc tttgtgatta ccattatggg tctgtgatg tgatcccacc1320
taattgtatc cagttaagaa atttgatcct gagtgccttt ccaagaaaca tgaggctccc1380
cgacccattc actcctaact taaagggtgga catgttgagt gaaattaaca ttgctccccg1440
gattctcacc aatttcactg gagtaatgcc acctcagttc aaaaaggatt tggattccct1500
tcttaaaact cgatcaccag tcacttctct gctgatctg cgcagaacct acaggatctc1560
aatgaacctg ggaatcgcta caacctccag ctcatcaatg cactgggtgc ctatgtcggg1620
actcaggcca ttgcgcacat ccacaacaag ggcagcacac cttcaatgag caccatcact1680
cactcagcac acatggatat cttccagaat ttggctgtgg acttgacac tgagggtcgc1740
tatctctttt tgaatgcaat tgcaaatcag ctccgggtacc caaatagcca cactcactac1800

ttcagttgca ccatgctgta ccttttttga gaggccaata cggaagccat ccaagaacag1860
atcacaaagag ttctcttggg acggttgatt gtaaataggc cacatccttg ggtctctctt1920
attaccttca ttgagctgat taaaaaccca gcgtttaagt tctggaacca tgaatttgta1980
cactgtgccc cagaaatcga aaagtatttc cagtccgtcg cacagtgtg catgggacag2040
aagcaggccc agcaagtaat ggaagggaca ggtgccagtt agacgaaact gcactctctg2100
tgtacgtgtc agtctagagg tctcactgca ccgagttcat aaactgactg aagaatcctt2160
tcagctcttc ctgactttcc cagccctttg gtttgggggt atctgcccc actactgttg2220
ggatcagcct cctgtcttat gtgggcacgt tccaaagttt aaatgcattt ttttgactct2280
tggccaaaat ttagaagatg ctgtgaatat cattttgaac ttgtgtaaat acatgaaaga2340
ggaaaacctt tgtctggaac ttcttggctt tgtgcaagct gtgtccaagg caagtacata2400
aactggtaac ttgtaatgaa gaggcagctg atgccatgca cttgtctgag ggcatagtct2460
catgtctctc gacattctcg gtgtcccaa aagccagttt gaattattatg2520
taacttattt ttttaattgg gacaggggac cttgaaaatc actaagttat taaaaatgtg2580
gatgtgctag aattggatat gtccaggaac atgggaaggg ctactattg gaatcccatg2640
agtctccatt ttgtctctac ccaaactgat tccaaagctg actgcatttg taccatctta2700
ttctctttgg ggattatata cctcagccgc ctgagatggg ggtcagctct ttatataaag2760
ggaaaaccaga ccaggcctaa agccccccc ctacccctac ccccccaca atcctctct2820
gaaactttta aaaccagtgg ggatttttag gaaagggaac ccaaaccgcg attaatgt 2878

```



## (2) INFORMATION ON SEQ ID NO. 68:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 701 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

```

atgatatttt ggatgtagtc ttttgattgt ttaaattctta aaaagtaatg ggatcttttg 60
acactggggg atgttttatt tttatgtgtg caaattttta ccatattctt ttctagttaa120
agaggaaaaa gcaagtgtgt ccagaaaaac ctgtaaagaa acaaaaagaca ggtgagactt180
cgagagccct gtcattctct aaacagagca gcagcagcag agatgataac atgtttcaga240
ttgggaaaaa gaggtacgtt agtggttcgcg attttaaagg caaagtgcct attgatatta300
gagaatattg gatggatcct gaaggtgaaa tgaaaccagg aagaaaaggt atttcttta360
atccagaaca atggagccag ctgaaggaac agatttctga cattgatgat gcagtaagaa420
aactgtaaaa ttcgagccat ataaataaaa cctgtactgt tctagtgttt ttaatctgtc480
tttttacatt ggcttttgtt ttctaaatgt tctccaagct attgtatgtt tggattgcag540
aagaatttgt aagatgaata ctttttttta atgtgcatta ttaaaaatat tgagtgaagc600
taattgtcaa ctttattaag gattactttg tctgccacc acctagtgtg aaataaaatc660
aagtaataca atcttaaaaa aaaaaaaaaa aaaagtcgag c 701

```

## (2) INFORMATION ON SEQ ID NO. 69:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 817 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

gttttttttt tttttttttt ttttttttaa gcacagaaaag cttttattac cacagaggaa 60
atcaggaaaat gctggaggga gcctcgtag ctgtgtgatc agggagggga cagcaggcgg120
gaacccgtca tcaatcatgt ctgggcagtc tcccaaccaa caggtttggt tggttcaggal80
gaggcttttg ctgggctgtg tgtgtgtatg atcaggaagg tcagcctcaa caaatgggct240
tcttcctgga cataggacag ccagaatcgg ggacaccagc tgcacagaca ccaccttaaa300
atggaaatca aattagggttc attacatcag gaagtacatt tcaccctgat cataaaagag360
ggacaaggga gcaactgggct ctactggata gcctttcttt tagataagat gcttttaaaa420
gttaaacatt ggcagggcct ttcccctagc taacagcaag cagcacacaa ttccaagtca480
gcttgtaaaag cttttgttat ctttgttatc tgttattatt tggattttga acgaaattga540
tggagtacga gccggttagag gaatcctgtt tgatctggaa attttccgtg gagagoccaa600
aaggtcggag aaccaagttc ccaagatctt ttaatttacc taacatctct tcttttagtc660
tttcattacg ttcttcaatt tgcttaggta atctcataca agcttctctt gcttgatgta720
ttgatgaagg ttcccgctg ctgtccctc cctgatcaca cagctaacga ggctcctcca780
gcatttctctg atttctctg tggtataaaa agctttc 817

```

(2) INFORMATION ON SEQ ID NO. 70:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 2686 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

```

gcaaggccta ctgtcggtcg ggaggggagg tgtagccggt ctttgggggt aggcggtagt 60
ggcggaaagag gttcggcggc tgatggcgga tcaggatcgg aagcctgcgt aactttctcc 120
cttgatccgg gagtctttcc actggattca caatgacatc ctttcaagaa gtcccattgc 180
agacttccaa ctttgcccat gtcattcttc aaaaatgtgg caagagttac cttcctaattg 240
cacacctgga atgtcattac accttaactc catatattca tccacatoca aaagattggg 300
ttggtatatt caaggttgga tggagtactg ctctgatta ttacacgttt ttatgggtccc 360
ctatgacctga acattatgtg gaaggatcaa cagtcaattg tgtactagca ttccaaggat 420
attaccttcc aaatgatgat ggagaatttt atcagttctg ttacgttacc cataagggtg 480
aaattcgtgg agcaagtaca ctttccagt ttctgagctt ttctccagtt gaagagctgc 540
ttactatgga agatgaagga aattctgaca tgttagtggg gaccacaaaa gcaggccttc 600
ttgagttgaa aattgagaaa accatgaaaag aaaaagaaga actgttaaaag ttaattgccg 660
ttctggaaaa agaaaacagca caacttcgag aacaagttgg gagaatggaa agagaactta 720
accatgagaa agaaaagatgt gaccaactgc aagcagaaca aaagggtctt actgaagtaa 780
cacaaagctt aaaaatggaa aatgaagagt ttaagaagag gttcagtgat gctacatcca 840
aagcccatca gcttgaggaa gatattgtgt cagtaacaca taaagcaatt gaaaaagaaa 900
ccgaattaga cagttttaaag gacaaactca agaaggcaca acatgaaaag gaacaacttg 960
aatgtcagtt gaagacagag aaggatgaaa aggaacttta taaggtacat ttgaagaata1020
cagaaataga aaataccaag cttatgtcag aggtccagac tttaaaaaat tttagtggga1080
acaaagaaaag cgtgattact catttcaaag aagagattgg caggctgcag ttatgtttgg1140
ctgaaaagga aaatctgcaa agaactttcc tgcttacaac ctcaagtaaa gaagatactt1200
gtttttttaa ggagcaactt cgtaaaagcag aggaacaggt tcaggcaact cggcaagaag1260
ttgtctttct ggctaaagaa ctcaagtgtg ctgtcaacgt acgagacaga acgatggcag1320
acctgcatac tgcacgcttg gaaaacgaga aagtgaaaaa gcagttagct gatgcagtg1380
cagaacttaa actaaatgct atgaaaaaag atcaggacaa gactgataca ctggaacacg1440
aactaagaag agaagttgaa gatctgaaac tccgtcttca gatggctgca gaccattata1500
aagaaaaatt taaggaatgc caaaggctcc aaaaacaaat aaacaaactt tcagatcaat1560
cagctaataa taataatgtc ttcacaaaga aaacggggaa tcagcagaaa gtgaatgat1620
cttcagtaaa cacagaccca gccactctg cctctactgt agatgtaaa ccatcacctt1680
ctgcagcaga ggcagatttt gacatagtaa caaaggggca agtctgtgaa atgaccaaag1740
aaattgctga caaacagaa aggtataata aatgtaaaca actcttgag gatgagaaag1800
caaaatgcaa taaatagtct gatgaacttg caaaaatgga gctgaaatgg aaagaacaag1860
tgaaaattgc tgaaaatgta aaacttgaa tagctgaaat acaggacaat tataaagaac1920
ttaaaggag tctagaaaat ccagcagaaa ggaaaatgga agatggagca gatggtgctt1980
tttaccaga tgaaatacaa aggccacctg tcagagtccc ctcttgggga ctggaagaca2040
atgttgtctg cagccagcct gtcgaaact ttagtcggcc tgatggctta gaggactctg2100
aggatagcaa agaagatgag aatgtgccta ctgctcctga tctccaagt caacatttac2160
gtgggcatgg gacaggcttt tgctttgatt ccagctttga tgttcacaag aagtgtcccc2220
tctgtgagtt aatgtttcct cctaactatg atcagagcaa atttgaagaa catgttgaaa2280
gtcactggaa ggtgtgccc atgtgcagcg agcagttccc tctgactat gaccagcagg2340
tgtttgaaag gcatgtgcag acccattttg atcagaatgt tctaaatttt gactagttag2400
tttttattat gagttaatat agtttagcag taaaaaaaa aaaaaaaacc acacctaaaa2460
tagaccactg aggagaccat agagcggatg ctttcatgca ccctttactg cactttctga2520
ccaggagcta ctttgagttt ggtgttacta ggatcagggt cagtctttgg cttatcaata2580
aattttaatc tctgttaatc ttacaaaaat taaaaaaaa aaaaaaaat cgtactttat2640
ttatccctag ttgcagactg ctgaataaag gtcaaggatt atccat 2686

```

## (2) INFORMATION ON SEQ ID NO. 72:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 922 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

ctgctctgaa aagccatctt tgcattgttc ctcatccgcc tccttgctcg cggcagccgc 60
ctccgccgcg cgctctctcc gccgccgcgg actccggcag ctttatcgcc agagtccctg120
aactctcgct ttctttttaa tccctgcat cggatcaccg gcgtgcccc aatgtcagal80
cgagccgcta gacaccagct ccgaaatcac caccaaggac ttaaaggaga agaaggaa240
tgtggaagag gcagaaaatg gaagagacgc ccttgctaac gggaatgcta atgaggaaa300
tggggagcag gaggctgaca atgaggtaga cgaagaagag gaagaagggg ggtgatggtg360
aggaagagga tggagatgaa gatgaggaag ctgagtcagc tacgggcaag cgggcagctg420
aagatgatga ggatgacgat gtcgatacca agaagcagaa gaccgacgag gatgactaga480
cagcaaaaaa ggaaaagtta aactaaaaaa aaaaaggccg ccgtgacctt ttcacctcc540
acttcccgtc tcagaatcta aacgtggtca ccttcgagta gagaggccc cccgccacc600
gtgggcagtg ccaccgcag atgacacgag ctctccacca cccaacccaa accatgagaa660
tttgcaacag gggagggaaa aaggaccaa acttccaagg ccctgctttt tttcttaaaa720
gtactttaaa aaggaaattt gtttgtatgt tctatttaca ttgatagtgt ttgtacatat780
tgtaggggt caaccatttt taatgatctc ggatgaccaa accagccttc ggaagcgttc840
tctggcctac ttctggactt ttacgttggt gggttgttga ccatgttcaa ttataatccc900
aaaaggggga aaaaaaacct tt                                     922

```

## (2) INFORMATION ON SEQ ID NO. 73:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 870 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

```

ggaagtggcg gtgcgagggc tgctgcacag cgagcggagc cgcggtccgg acggcagcgc 60
gtgccccgag ctctccgcct ccccccgccc gccagccgag gcagctcgag cccagtcgcg 120
ggccccagca gcagcgccga gacgagcccc agtagcagcg ccatggccgg gtggaacgcc 180
tacatcgaca acctcatggc ggacggggacc tgtcaggacg cggccatcgt gggctacaag 240
gactcgccct ccgtctgggc cgcggtcccc gggaaaacgt tcgtcaacat cacgccagct 300
gaggtgggtg tcctggttgg caaagaccgg tcaagttttt acgtgaatgg gctgacactt 360
ggggggccaga aatgttcggt gatccgggac tcaactgctg aggatgggga atttagcatg 420
gatcttcgta ccaagagcac cgggtggggcc cccaccttca atgtcactgt caccaagact 480
gacaagacgc tagtcctgct gatggggcaaa gaaggtgtcc acggtgggtt gatcaacaag 540
aaatgttatg aaatggcctc ccaccttcgg cgttcccagt actgacctcg tctgtccctt 600
ccccctcacc gctccccaca gctttgcacc cctttcctcc ccatacacac acaaaccatt 660
ttattttttg ggccattacc ccataccctt tattgctgcc aaaaccacat gggctggggg 720
ccagggctgg atggacagac acctccccct acccatatcc ctcccgtgtg tggttggaaa 780
acttttgttt tttgggggtt tttttttctg aataaaaaaa attctactta acaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaaggggggg

```

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1418 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

ataaaagagg aaagagtgcc caggtcttca ctccactgcg actgcagaac tcagagctgc 60
tcttcctctg tggccagttg gggaccagca tcatgaagtg gatggtggtg gtcttgggtc 120
gcctccagct cttggaggca gcagtgggtc aagtgtccct gaagaaattt aagtctatcc 180

gtgagaccat gaaggagaag ggcttgctgg gggagtctct gaggaccac aagtatgatc 240
ctgcttgga gttaccgctt ggtgacctca gcgtgacctc cgagcccatg gcttacatgg 300
atgctgccta ctttgggtgag atcagcatcg ggactccacc ccagaacttc ctggctcttt 360
ttgacaccgg ctctccaac ttgtgggtgc cctctgtcta ctgccagagc caggcctgca 420
ccagtcactc ccgcttcaac cccagcgagt cgtccacctc ctccaccaat gggcagacct 480
tctccctgca gtatggcagt ggcagcctca ccggcttctt tggctatgac accctgactg 540
tccagagcat ccaggtcccc aaccaggagt tcggcttgag tgagaatgag cctgggtacca 600
acttcgtcta tgcgcagttt gatggcatca tgggcctggc ctacctgct ctgtccgtgg 660
atgaggccac cacagctatg cagggcattg tcaggagggg cgcctcacc agccccgtct 720
tcagcgtcta cctcagcaac cagcagggtc ccagcggggg agcggttgtc tttgggggtg 780
tggatagcag cctgtacacg gggcagatct actgggcgcc tgtcaccacg gaactctact 840
ggcagattgg cattgaagag ttctcatcg gcggccaggc ctccggctgg tgttctgagg 900
gttgccaggc catcgtggac acaggcacct ctctgctcac tgtgccccag cagtacatga 960
gtgctcttct gcaggccaca ggggccagg aggatgagta tggacagttt ctcgtgaact 1020
gtaacagcat tcagaatctg cccagcttga ccttcacat caatggtgtg gaggctccct 1080
tgccaccttc ctcttatatc ctacagtaaca acggctactg caccgtggga gtcgagccca 1140
cctacctgtc ctcccagaac ggccagcccc tgtggatcct cggggatgtc ttcctcagg 1200
cctactatc cgtctacgac ttgggcaaca acagagtagg ctttgccact gccgcctaga 1260
cttgctgctc cgacacgtgg gctccccctc tcctcttgac cctgcacctc cctagggc 1320
tgtatctgtc tttccactct ggattcagcc ttctttttct ggactctgga ctttctctaa 1380
taataaatag ttcttctttt aaaaaaaaaa aaaaaaaa 1418

```

**(2) INFORMATION ON SEQ ID NO. 76:**

**(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH:** 1712 base pairs
- (B) TYPE:** Nucleic acid
- (C) STRAND:** individual
- (D) TOPOLOGY:** linear

**(ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing

**(iii) HYPOTHETICAL:** NO

**(iii) ANTI-SENSE:** NO

**(vi) ORIGIN:**

- (A) ORGANISM:** HUMAN
- (C) ORGAN:**

**(vii) OTHER ORIGIN:**

- (A) LIBRARY:** cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

gtggcagaaa acctcatgac acaatctctc cgctccctg tgttggtgga ggatgtctgc 60
agcagcattt aaattctggg agggcttggg tgctcagcagc agcaggaggg gcagagcaca 120
gcatcgtcgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca aacgccgacc 180
aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctccta ggcatcacct 240
gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag ctttacaaca 300
aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag cagaatctcc 360
tagccccaca gaatgctgtg tctctgaag aaaccaatga ctttaaaaaa gagacccttc 420
caagtaagtc caacgaaagc catgaccaca tggatgatat ggatgatgaa gatgatgacg 480
accatgtgga cagccaggac tccattgact cgaacgactc tgatgatgta gatgacactg 540
atgattctca ccagtctgat gagtctcacc attctgatga atctgatgaa ctggtcactg 600

atcttccac ggacctgcca gcaaccgaag ttttcaactc agttgtcccc acagtagaca 660
catatgatgg ccgaggatgat agtgtggttt atggactgag gtcaaaatct aagaagtttc 720
gcagacctga catccagtac cctgatgcta cagacgagga catcacctca cacatggaaa 780
gcgaggagtt gaatgggtgca tacaaggcca tccccgttgc ccaggacctg aacgcgcctt 840
ctgattggga cagccgtggg aaggacagtt atgaaacgag tcagctggat gaccagagtg 900
ctgaaaacca cagccacaag cagtccagat tatataagcg gaaagccaat gatgagagca 960
atgagcattc cgatgtgatt gatagtcagg aactttccaa agtcagccgt gaattccaca1020
gccatgaatt tcacagccat gaagatatgc tggttgtaga ccccaaaaagt aaggaagaag1080
ataaacacct gaaatttctt atttctcatg aattagatag tgcattctct gaggtcaatt1140
aaaaggagaa aaaatacaat ttctcacttt gcatttagtc aaaagaaaaa atgctttata1200
gcaaaatgaa agagaacatg aaatgcttct ttctcagttt attggttgaa tgtgtatcta1260
tttgagtcct gaaataacta atgtgtttga taattagttt agtttggtgc ttcatggaaa1320
ctccctgtaa actaaaagct tcagggttat gtctatgttc attctataga agaaatgcaa1380
actatcactg tatttttaata tttgttattc tctcatgaat agaaatttat gtagaagcaa1440
acaaaatact tttaccact taaaaagaga atataacatt ttatgtcact ataattcttt1500
gttttttaag ttagtgtata tttgttgctg attatctttt tgtggtgtga ataaatcttt1560
tatcttgaat gtaataagaa tttggtgtg tcaattgctc atttgtttcc ccacggttgt1620
ccagcaatta ataaaacata acctttttta ctgcctaaaa aaaaaaaaaga gaaaagaaaa1680
aaaagaaaag aaaaaaaggg gagggagggg ag
1712

```

## (2) INFORMATION ON SEQ ID NO. 78:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

```

accgcccccg ctgtgggtct cagcagctcg ggcggcgggg ggggtggcag cggcaaggca 60
gcccagtttc gcgaaggctg tcggcgcgcc gcggcccgca ggcacccggc acgcgccttc 120
cccgcaggca cccggcacgc gccttccccg ccgccacgat gcccaagagg aaggtcagct 180
ccgcccgaagg gccgccaagg aagagcccaa gaggagatcg gcgcggttgt cagctaaacc 240
tcttgcaaaa gtggaagcga accgaaaaag gcagcagcga aggataaatc ttcagacaaa 300
aaagtgcaaa caaaagggaa aaggggagca aagggaaaac aggccgaagt ggctaaccaa 360
gaaactaaaag aagacttacc tgcggaaaac ggggaaacga agactgagga gagtccagcc 420
tctgatgaag caggagagaa agaagccaag tctgattaat aaccatatac catgtcttat 480
cagtggctcc tgtctccctt cttgtacaat ccagaggaat atttttatca actattttgt 540
aaatgcaagt tttttagtag ctctagaaac atttttaaga aggagggaat cccacctcat 600
cccatttttt aagtgtaaat gctttttttt aagaggtgaa atcatttgct ggttggttat 660
tttttggtac aaccagaaaa tagtgtggga tattgaatta tgggaggctc tgactgtctc 720

```

```

gggtgtcagc ttaacattcc acagatgggg ggtagtttt tatatcctat aatacaaaagc 780
atattaaaatg gcaatatgga gtcagtcctg catttaatgt cttgaacatt ttaaattact 840
tctattacca tgttggtttt tagtagaatt gtttcctaaa gaaaaccact ctttgatcat 900
ggctctctct gccagaattg tgtgcactct gtaacatctt tgtggtagtc ctgttttcct 960
aataactttg ttactgtgct gtgaaagatt acagatttga acatgtagtg tacgtgctgt 1020
tgagttgtga actggtgggc cgtatgtaac agctgaccaa cgtgaagata ctggtaactg 1080
atagcctctt aaggaaaatt tgcttccaaa ttttaagctg gaaagtcact ggaataactt 1140
taaaaaagaa ttacaatata tggcttttta gaatttcgtt acgtatgtta agatttgtgt 1200
acaaattgaa atgtctgtac tgatcctcaa ccaataaaat ctcagttatg aaaataaaaa 1260
aaaaaaaaaaa aaa                                     1273

```

## (2) INFORMATION ON SEQ ID NO. 79:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2342 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

```

cctcggacca cgggactggc ctggggcggg acgtggggcg gggggcgcg cgtgcggcac 60
gctgcagggc tgaagcggcg gcggcggtgg ggactgcacg tagcccgcg ctgggcatgg 120
ctctcctggt gctcgggtctg gtgagctgta ccttctttct ggcaagtgaat ggtctgtatt 180
cctctagtga tgatgtgatc gaattaaact catcaaattt caaccgagaa gttattcaga 240
gtgatagttt gtggcttgta gaattctatg ctccatgggtg tggtcactgt caaagattaa 300
caccagaatg gaagaaagca gcaactgcat taaaagatgt tgtcaaagtt ggtgcagttg 360
atgcagataa gcatcattcc ctaggaggtc agtatgggtg tcagggattt cctaccatta 420
agatttttgg atccaacaaa aacagaccag aagattacca agtgggcaga actgggtgaag 480
ccattgtaga tgctgcgctg agtgctctgc gccagctcgt gaaggatcgc ctcgggggac 540
gaagcggagg atacagttct ggaaaacaag gcagaagtga tagttcaagt aagaaggatg 600
tgattgagct gacagacgac agctttgata agaattgtct ggacagtga gatgtttgga 660
tggttgagtt ctatgctcct tgggtgtggac actgcaaaaa cctagagcca gagggtgtg 720
ccgcagcttc agaagtaaaa gagcagacga aaggaaaaagt gaaactggca gctgtggatg 780
ctacagtcaa tcaggttctg gcctcccgat acgggattag aggatttctt acaatcaaga 840
tatttccagaa aggcaggtct cctgtggatt atgacgggtg gcggacaaga tccgacatcg 900
tgtcccgggc ccttgatttg tttctgata acgccccacc tcctgagctg cttgagatta 960
tcaacgagga cattgccaa aggacgtgtg aggagcacca gctctgtgt gtggtgtgtc 1020
tgccccatat ccttgatact ggagctgcag gcagaaattc ttatctggaa gttcttctga 1080
agttggcaga caaatacaaa aagaaaatgt ggggtggct gtggacagaa gctggagccc 1140
agtctgaact tgagaccgcg ttggggattg gaggttttgg gtaccccgcc atggccgccal 1200

tcaatgcacg caagatgaaa tttgctctgc taaaaggctc cttcagtga caaggcatca 1260
acgagtttct cagggagctc tcttttgggc gtggtctcac ggcacctgta ggagcgggg 1320
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aggatgacat tgacctcagt gatgtggagc ttgatgactt agggaaagat gagggtgtga 1440
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gtgaagggac attctctaca ctacagatgac tctaccagtg gccttttaac caagaagtag 1560
tacttgattg gtcatttgaa aacactgcaa cagtgaactt ttgcatctca agaaaacatt 1620
gaaaaattct atgaattggt gtagccgggtg aattgagtcg tattctgtca cataatat 1680
tgaagaaaac ttggctgtcg aaacattttt ctctctgact gctgcttgaa tgttcttgg 1740
ggctgtttct tatgtatggg ttttttttaa tgtgatccct tcatttgaat ataatggct 1800
ttttccatta aagaataaaa ttttttggac aatgccgata aatgtatgaa gttagtatcc 1860
acatcataaaa ttcagagtga tgtttagcag taaatcaata tttgaagtg atacacagat 1920
gtttttcttc cccacaaaact tttttaaaca aaaaacaaga cctcttttct ttagatgggt 1980
ccacctatgc ccaccacaac agagatttta catggaaacc gggctcagtg agaactgatt 2040
tcttgcccaa tatttgtctt tgggtgtgtc ctagtgaacta attattaagg aatctagctg 2100
gttatacagt tcaaggcttt ctatgttgtt aatgaacctc aaaatagccg ttaagacatg 2160
aaatacacga gcaggttacc aatgcgaaca ggtagtctgc atttatgtaa aacattcaga 2220
aaatgaagtt ttgaatttgt tggaacattc aaaggacttg agagcatttt attgtaactt 2280
aaaaaaaaaa atacaactgt cactaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2340
aa

```

## (2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 1959 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

```

gcagttatat aataagtttg ggagacaaaa tgatacgcac acgagagaag atgaagaaga 60
tactcaaagt tccaaatctg aagaacatca tttgtactct aatccaatca aagaagaaat 120
gactgagtct aagttctcta agtactctga aatgagtgag gaaaaacgag ccaaacttcg 180
tgaaattgag ctcaaagtta tgaagtttca ggatgaattg gaatctggga aaagacctaa 240
aaaaccaggc cagagttttc aggagcaagt agaacactac agagataaac ttcttcaacg 300
agagaaagag aaagagttag aaagagaacg agaaagagac aagaaagata aagaaaaatt 360
ggaatctcgc tccaaagaca agaaggaaaa agatgagtggt actccgacaa ggaaggaaaag 420
gaagaggcga cacagtacat cccccagccc atctcgcagt agcagtggtg gacgagtgaa 480
atccccatca ccaaaatcgg agcgatcaga gcgttcagaa agatctcata aagagagctc 540
acgggtccagg tcatctcaca aagattctcc tagagatggt agcaaaaaag ccaaaagatc 600
accatctggt tcaaggacac ctaaaaggtc taggcgatca cggctctagat ctcttaaaaa 660

```

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atcaggaaaag aagtccagat ccaggtccag atctccacac aggtctcata aaaagtcaaa 720
gaaaaacaaa cactgacgta aatttttaag atgctgtcac ttattggaaa tgcgatttgt 780
tttgtgcctg aacgggtctgt tttttaaaaa aacaaaaaat caaatgaaaag agcattcctg 840
gggttttttg tttgttttg tttgtcatgtg taaactcatg agcaactgca tctgtagatc 900
tgtcattggt ttatattgtg taaattactt tcattgtggc tatttctcaa gatgaaattt 960
ttattgttct aatggatttc atcagaaatg tgtataatgg atctgctgac agtagtagta 1020
ttttgtttta ggatgttggt acttagcaaa aataatacag atgtcttccc cccttttgta 1080
gctttgacaa tttgaattag atttcaata aaatctgaac agaaaaacta aatgttgttt 1140
ttttgcccc aagggtgat taagtcctt aaagtcctac tgagtttcac actactgttg 1200
tgcttcttat acctgatgca ctttataagc ccagtggtc aagtagctta agttttatat 1260
ttactaagat gactatccaa attaaggagc ctgagactcc tatttggttg tttgctaacc 1320
atltgctttt gataagtttc tcttggttaa tactaatacc cagatatcaa agactaggtal 1380
gatattggcat ggcggtttgt tagtggaatg cctggctaaa acattttttt cacagaagca 1440
atatgatatt catacatcca acccatgttc tgagcaacta cttactttta gggggaaaat 1500
aaatatcttt tcatctctc ttctattatg aaagaagttt atttgtaaaa caaattttct 1560
aacaaggttt ggccatagaa ttctcttgta tgattgttga ctttttataa tcttctgtag 1620
gctatctttt aaacactggc atcagaatat tttttataag tttgtgttta aacagcttag 1680
ttggtcccc ccccccactc caagagactt ggggttagtt atagcttta gtaaaattal 1740
aaaaataaat gtttttcagg aaacttcgta tctaattggt tgtaaatcca aggtgcaaaa 1800
agttgattta aaccatttgc agagttgaac tctattatga aaataaattt gctacggtat 1860
gaggaagaaa taaaacttgt gtaatgttgg tcataatact gctataaata taataaaggg 1920
ttatgtagaa ttgaactgac aaaaaaaaaa aaaaaaaaaa 1959

```

## (2) INFORMATION ON SEQ ID NO. 81:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3708 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

gccoctatta tcacgcacgg tagacaagct tttttttttt ttttttttta cagcttataa 60  
 cacaactttt attagaaaaa ttatacataa catagcatca actattttca agaacaatat 120  
 taaacccgat aagcaacaaa aaccagacta acaaaatgtg taacaagaaa ctaatgacct 180  
 ttctaaaatc aaacattcaa ttatctacaa tgtcttttta caaacgggga aaactccttg 240  
 gtttacaggc acatcatatt gaataaaaag ctgcaatagc aattttatac aattaccact 300  
 ctgaagaaac tgaatcatta aaacagtaat tacgagttca caaattttaa acatttcaca 360  
 taatttttaa ttattgggta tacactgaag tctgagtttc aaaagtgatt tttttttccc 420  
 acaaaagttt caacacttaa gctagaactt tcagtgttaa ctttgcccta aaaagttaag 480  
 acatattctg ataatacataa cagtcacatg atttctgatg ctatctggtc tgtaataat 540

aaagctcttta tttggatgta tttttcttca attaaattac aggaaactgg atataggatt 600  
 tcgttgcaac gctattaaaag ttccaaacca ggagtgtgca gcactggaaa aggagatcag 660  
 tactaaaaat tacaataaat atcagagaag ccgttagttt ttacagcatc gtctgcttaa 720  
 aagctaagtt gaccaggtgc ataatttccc atcagtctgt ccttgtagta ggcagggcaa 780  
 tttctgtttt catgatcgga atactcaaat atatccaaac atctttttta aactttgatt 840  
 tatagctcct agaaaattat gttttttaat agtcaactca ctctaactcag gctagctttt 900  
 gctcattttg gagcctcact aaaataacag atttcagtat agccaagtgc atcagaaaga 960  
 ctcaaatgga atgatttaca aaatagaaca ctttaaaacca ggtcagtcct atctttttgt 1020  
 agctgaaggc tatcagtcac aacacaattt cgcgtacacc tctgctcatt atggaattac 1080  
 acttaaaacg aatctcaaga ggggtgacct tgtgttttca gataccatcc ctaaggagag 1140  
 tgggttaacag gaagattgcc agtgtttact atggaaagaa gtgtttgttt gttttttttt 1200  
 cttgtcaaaag acttacacca tagtttttaa ttaactgtc aggcattttc tcagacaggt 1260  
 tttccttttc aatgcagtaa tgaagaacta agataaaaaat catgactttt gactgccact 1320  
 caacattatt acatgcacca atattgcaca catctgttct gaactgttaa aatcatcttc 1380  
 tgagtccttg ggggtgctgtt ttctccatca gaacacaaac acaaccatc taatcagttt 1440  
 ccctcaaaga tgaaattgac aaatttaatg tactggaaaa aaatgaagaa ggaaaaaggc 1500  
 aaagactttg tacagacaaa aatctaagtt ttctcaaagg gttctgtgtc ccttacacat 1560  
 gggggcaatt tgtaagcact agtgaatcaa acactagcta taatgcttct agctccttat 1620  
 ataatatgga accttggtcc aggtgttgcg atgatgtcac tgaacggttc ttctgtgtc 1680  
 agctcaatag cttgctgctt ttaagaacc aagaagctgt agaactttgc ggcagcttgt 1740  
 tttctgttcg tatctcgaca taactcaagc aaactgatag attcagctcc agttttagca 1800  
 agagcacgct gaagaccatg aagcatctgc tgagtccttt tgttccatc ttctttttcc 1860  
 tgatcttgat cgccccctga tgcattctca tctcttccct ctccatcctc ttctttttcc 1920  
 ttctctttct cctctctctt ttctggcaga agttctaaact ctggtattag ctgacagata 1980  
 tttggagggt cttctggggg aagctctaca ggtgggtatt ccctctgct ctgggtcaat 2040  
 ttgtccagct ttctgcttaa ctccctgagg tgggtgggtgga ggcataagct actcatctat 2100  
 gtttgtttctg ctggcctcca tcaatgactc ctggaggcgg cttggctcct caataatggg 2160  
 ctcatcgata acatcacgct cctgatgctg ctgttgctgg tctctctag gaacctctgg 2220  
 attttcaaat tctttgagga attcatccaa attatctgcc tctcctcctt tctcctttt 2280  
 tctaaggtct tctggtacaa gcggtgtaag acagcgtgta aagagcttca gtagtctgtt 2340  
 attccacaaa ggcgtgagcag gtaaaagaaa cagtttttct actcctcctg tctctttcca 2400  
 catcatcaat ttcttggtgg cgggtgccga tccaaagtag taacaatac tgaataatca 2460  
 ctaagttggg ctctaattgt cttgctatcc aactctttga cactgtcaac aattagcttc 2520  
 ctcttctctt tggcttttgt ttctttaaca gttatatcaa taggctcaa tgcaaatgct 2580  
 tcttctcat ttggaacaag tgtgtttga tcagtcaggg ttggcattgg ttcaacggga 2640  
 tccactgaat caggactatc aggccacccc attgatacat tatcatctc atccatatcg 2700  
 tcatgtgcag gctgctctgg caacatcacc cctgcctcag agagggcagg gggatcatca 2760  
 aagataccgc catcattatt actaataagt ttgtcatcta atattccacc atcatttctc 2820  
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 agattgctgg tgctctgttc agactctaag aggaggttag aagtagtagt gcttactaac 2940  
 atgtcgtcat cctcaaaagc actgccttct ctcatctat cactgatcct cattccaaaa 3000  
 tcacaaaaat cattttcttg taaaatactg atgttcccaa cttcttctct catggttatc 3060  
 tcttccactc tactctgatt caagctgaac tgctgggcca catcgatgtc atctaagtc 3120  
 ggcagtggct gatcaaagtc atgaaattct tcaggtaaaag taatggcatt ataagctgct 3180  
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 aatgcttcat tacagtctgc aagaaggtat ttggctttcc tgtgatagat tcgaactact 3300  
 cccagtaaga gatgtcctga tgtccgtaat gccattttta cctttgggtga gatgatactc 3360  
 ttccacgctg ctctctaaat tacactcgaa cacatgggct ttgggttagct tcttatccca 3420  
 atgggcccgt agccaaattc ttgccagagg cctcttttta ctgagaacaa aatgtgcgta 3480  
 gaacattggt ctggctggct atgaaaacag aagaaaacct tgctctccgc tgggagttgg 3540  
 gcgggctggg tggcccgggg aggggaaaag ggtcggggga ggggggggg aaagggggga 3600  
 gcccttgcca ggtgtagctt ccgagcagct ccccgccccc cacagccggc gctccttccc 3660  
 cgattcactc aaacaaacaa gatggctgcc gtaacccgc ggctcttc 3708

## (2) INFORMATION ON SEQ ID NO. 82:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3045 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```

gtccattgcc caaaatccgc tatgaaagct tgaccaatcc ccagtaaatt agacctctgg 60
gaaaagagct gccatattac ccatacccca aacaaccaag atcgaaactct cactattgtg 120
gatactggaa ttggaatgac caaggctgac ttgatcaata accttggtac tatcgccaag 180
tctgggacca aagcgttcat ggaagctttg caggctggtg cagatatctc tatgattggc 240
cagttcgggtg ttggttttta ttctgcttat ttggttgctg agaaagtaac tgtgatcacc 300
aaacataacg atgatgagca gtacgcttg gagtccctcag cagggggatc attcacagt 360
aggacagaca caggtgaacc tatgggtcgt ggaacaaaag ttatcctaca cctgaaagaa 420
gaccaaactg agtacttgga ggaacgaaga ataaaggaga ttgtgaagaa acattctcag 480
tttattggat atcccattac tttttttgtg gagaaggaac gtgataaaga agtaagcgat 540
gatgaggctg aagaaaagga agacaaagaa gaagaaaaag aaaaagaaga gaaagagtcg 600
gaagacaaac ctgaaattga agatgttggg tctgatgagg aagaagaaaa gaaggatggg 660
gacaagaaga agaagaagaa gattaagaa atgtacatcg atcaagaaga gctcaacaaa 720
acaaagccca tctggaccag aaatcccgac gatattacta atgaggagta cggagaattc 780
tataagagct tgaccaatga ctgggaagat cacttggcag tgaagcattt ttcagttgaa 840
ggacagttgg aattcagagc ccttctattt gtcccacgac gtgctccttt tgatctgttt 900
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tctcaaaatc ggaagaagct ttcagagctg ttaagggtact acacatctgc ctctgggtgat 1260
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atcatgaaag ctcaagccct aagagacaac tcaacaatgg gttacatggc agcaaaagaa 1740
cacctggaga taaaccctga ccattccatt attgagacct taaggcaaaa ggacagggct 1800
gataagaacg acaagtctgt gaaggatctg gtcattctgc tttatgaaac tgcgctcctg 1860
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aaacttgggtc tgggtattga tgaagatgac cctactgctg atgataccag tgctgctgta 1980
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ttttcaagga tgtttttctt ttttttgggt aatattaaaa agtctgtatg gcatgacaac 2160
tactttaagg ggaagataag atttctgtct actaagtgat gctgtgatac cttaggcact 2220
aaagcagagc tagtaatgct ttttgagttt catgttggtt tattttcaca gattggggta 2280
acgtgcactg taagacgtat gtaacatgat gttaactttg tgtggtctaa agtgtttagc 2340
tgtcaagccg gatgcctaag tagaccaaat cttgttattg aagtgttctg agctgtatct 2400

tgatgtttag aaaagtattc gttacatctt gtaggatcta ctttttgaac ttttcattcc 2460
ctgtagttga caattctgca tgtactagtc ctctagaaat aggtttaaact gaagcaactt 2520
gatggaagga tctctccaca gggcttgggt tccaaagaaa agtattgttt ggagagcaaa 2580
agttaaaaagc ctacctaagc atatcgtaaa gctgttcaaa aataactcag acccagctct 2640
gtggatggaa atgtagtgtc cgagtcacat tctgcttaaa gttgtaacaa atacagatga 2700
gttaaaagat attgtgtgac agtgtcttat ttagggggaa aggggagtat ctggatgaca 2760
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gcacagaaaa caggaatgca gacaacatgc atcccctgcg tccatgagtt acatgtgttc 2940
tcttagtgtc caogttgttt tgatgttatt catggaatac cttctgtgct aaatacagtc 3000
acttaattcc ttggccaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3045

```

## (2) INFORMATION ON SEQ ID NO. 83:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2815 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```

cagtggcggc gcaaccagcc ttctagggcg gcgaggaggt ggagtcaaca tatcaatgga 60
gcaagtcaca gtcgtcgatg ccagcttctt cttgaaatct acccagaatg gaatcctgac 120
aatgatacag gacacacaat gggatgatcca ttcattgttc agcagctctac aaatccagca 180
ccaggaattc tgggacctcc acctccctca ttctatcttg ggggaccagc agttggacca 240
agaggaaatc tgggtgctgg aaatggaaac ctgcaaggac ctagacacat gcagaaaggc 300
agagtggaaa ctagcagagt tgttcacatc atggattttc aacgagggaa aaacttgaga 360
taccagctat tacagctggt agaaccattt ggagtcattt caaatcatct gattctaaat 420
aaaattaatg aggcattttat tgaaatggca accacagagg atgctcaggc cgcagtggaat 480
tattacacaa ccacaccagc gttagtattt ggcaagccag tgagagtcca tttatcccag 540
aagtataaaa gaataaagaa acctgaagga aagccagatc agaagtttga tcaaaagcaa 600
gagcttggtgac gtgtgataca tctcagcaat ttgccgcatt ctggctattc tgatagtgtc 660
gttctcaagc ttgctgagcc ttatgggaaa ataaagaatt acatattgat gaggatgaaa 720
agtcaggtct ttattgagat ggagacaaga gaagatgcaa tggcaatggt tgaccattgt 780
ttgaaaaaag ccttttggtt tcagggggaga tgtgtgaagg ttgacctgtc tgagaaatat 840
aaaaaactgg ttctgaggat tccaaacaga ggcattgatt tactgaaaaa agataaatcc 900
cgaaaaagat cttactctcc agatggcaaa gaatctccaa gtgataagaa atccaaaact 960
gatggttccc agaagactga gagttcaacc gaagtaaaga acaagaagag aagtccggtg 1020
aagatggtga gaaagacaca aaggatgacc agacagagca ggaacctaat atgttcttg 1080
aatctgaaga tgagctactt gtatggaag aagaagcagc agcactgcta gaaagtggc 1140
gttcagtggg agacgagacc gatcttgcta atttaggtga tgtggcttct gatgggaaa 1200

aggaaccatc agataaagct gtgaaaaaag atggaagtgc ttcagcagca gcaaagaaaa 1260
agcttaaaaa ggtggacaag atcgaggaaac ttgatcaaga aaacgaagca gcgttgga 1320
atggaattaa aaatgaggaa aacacagaac cagggtgctga atcttctgag aacgctgat 1380
atcccaacaa agatacaagt gaaaacgcag atggtcaaaag tgatgagaac aaggacgact 1440
atacaatccc agatgagtat agaattggac catatcagcc caatgttctt gttggtatag 1500
actatgtgat acctaaaaa gggttttact gtaagctgtg ttactctttt tatacaaat 1560
aagaagttgc aaagaatact cattgcagca gccttctctc ttatcagaaa ttaaagaaat 1620
ttctgaataa attggcagaa gaacgcagac agaagaagga aacttaagat gtgcaaggag 1680
atttaatgat ttcaaagaaa ataattggtt tttgttttta atgttaacct ttttaaaata 1740
caatactgat agttagaaga aaactattgt actcttttgt tttagtggag aaataatag 1800
tgtctgttca tgtgttaagt gttatagcaa aaaaaataca catatgggta agttaatga 1860
tagtttttgt tttatcagaa tggcaacaga cagaagtact ttgtagagat tgacttcc 1920
agctacttaa gacaacttgc accactaaga aaaaaatgta gaaccatttg gaaaaatga 1980
atttagtagt tccaagtttc aaagaaatgt caacatttta ttccattcaa taaagaacaa 2040
aaccaatagt gtttttatta ctttcatctg aaacattcca tgttttaatc tgagccttg 2100
agactttcat ttggagtttg aaccctgttt ggttgcaatt catttttggg gaacttaatt 2160
aacgtgagat tggcaattga aatgcagggt cagttttctg ttaatgtcat gctgtgtgt 2220
aggtaataag aaatattaag taattggctt tagattttgt aattttttt cctgagttcc 2280
tgctagattt cgtatttctag tagtcaatgt attttcagtg aaatgcaaaa atattcccat 2340
tatctttgac cagtattaat ttttgagatc ttactgcttg tcaactgaaat cccgtgattg 2400
tcatacatct ctggtataag caacatttga ttttgaaagt gtgtagacca tctcttcata 2460
ttttcaagat gtaattttac atttctgcat ttttaaaaca gtttggccat aatcctagat 2520
gcacgcttct aattcatgta cctgcacatg tgacctttgt gaacagaaat ttgcatgtat 2580
aatttgtgtt tacttgtaac tttctggtta tatactgctt atatctgttg attcaagtta 2640
ctgaagtga taccaataaa aagaaaaccc taggccatgt taattgggta tacatgtttg 2700
gaatgttaac caaaaaaaa aacagtgtg gtttttattc gctcttaaac tttgtgcatg 2760
ctttaacaat ttatcgcttt taaatctaga gtgaattcct aaagagctgc cgcta 2815

```

## (2) INFORMATION ON SEQ ID NO. 84:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3462 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

ctggatcgta caagaaggga gacaaggacc actgacaaga taaggcctag caggaaacga 60  
 agcggctctt tccgctatct gccgcttgtc caccggaagc gagttgagac acggcagggt 120  
 cccgcccggg agaagcgacc aaagcgccctg aggaccggca acatggtgag gtcggggaat 180

aaggcagctg ttgtgctgtg tatggacgtg ggctttacca tgagtaactc cattcctggg 240  
 atagaatccc catttgaaca agcaaaagaag gtgataacca tgtttgtaca gcgacagggtg 300  
 ttgtctgaga acaaggatga gattgcttta gtctgtttg gtacagatgg cactgacaat 360  
 cccctttctg gtggggatca gtatcagaac atcacagtgc acagacatct gatgctacca 420  
 gattttgatt tgctggagga cattgaaagc aaaatccaac caggttctca acaggctgac 480  
 ttctggatg cactaatcgt gagcatggat gtgattcaac atgaaacaat aggaaagaag 540  
 ttgagaaga ggcatattga aatattcact gacctcagca gccgattcag caaaagtcag 600  
 ctggatatta taattcatag cttgaagaaa tgtgacatct cctgcaatt ctctctgctt 660  
 ttctcacttg gcaaggaga tggaagtggg gacagaggag atggccctt tcgcttaggt 720  
 ggccatgggc ctctcttcc actaaaagga attaccgaac agcaaaaaga aggtcttgag 780  
 atagtgaaaa tggatgatgt atcttttaga ggtgaagatg ggttgatga aatttattca 840  
 ttcaagtgaga gtctgagaaa actgtgctgc ttcaagaaaa ttgagaggca ttccattcac 900  
 tggccctgcc gactgacctt tggctccaat ttgtctataa ggattgcagc ctataaatcg 960  
 attctacagg agagagttaa aaagacttgg acagttgtgg atgcaaaaac cctaaaaaa1020  
 taagacatag tggccatagt tcgatatgct tatgacaaaa gagctaatac tgaagtttal1080  
 aaagaggata ttattcaagg gttccgctat ggaagtgaat tagttccttt ctctaaagtgl1140  
 gatgaggaac aaatgaaata taaatcggag ggaagtgtct tctctgtttt gggattttgt1200  
 aaatcttctc aggttcagag aagattcttc atgggaaatc aagttctaaa ggtctttgca1260  
 gcaagagatg atgaggcagc tgcagttgca ctctctctcc tgattcatgc ttggatgac1320  
 ttacacatgg tggccatagt tcgatatgct tatgacaaaa gagctaatac tcaagtctggc1380  
 gtggcttttc ctcatatcaa gcataactat gagtgtttag tgtatgtgca gctgctttcl1440  
 atggaagact tgcggcaata catgttttca tccttgaaaa acagtaagaa atatgctccc1500  
 accgaggcac agttgaatgc tgttgatgct ttgattgact ccatgagctt ggcaaaagaa1560  
 gatgagaaga cagacacctt tgaagaactg ttccaacca ccaaaatccc aaatcctcga1620  
 ttctcagagt tatttcagt tctgctgcac agagctttac atcccggga gctctacccl1680  
 ccaattcagc agcatatttg gaatatgctg aatctctccg ctgaggtgac aacgaaaagt1740  
 cagattcctc tctctaaaat aaagacctt ttctctctga ttgaagccaa gaaaaaggat1800  
 caagtgactg ctccaggaaat ttccaagac aacctgaag atggacctac agctaaaaaa1860  
 ttaaagactg agcaaggggg agcccacttc agcgtctcca gtctggctga aggcaggtct1920  
 acctctgttg gaagtgtgaa tctgtctgaa aacttccgtg ttctagttaa acagaagaag1980  
 gccagctttg aggaagcgag taaccagctc ataaatcaca tcgaacagtt ttgggatact2040  
 aatgaaacac cgtattttat gaagagcata gactgcattc gagccttccg ggaagaagcc2100  
 attaaagttt cagaagagca gcgctttaac aacttctctga aagcccttca agagaaaagt2160  
 gaaattaaac aattaaatca ttcttgggaa attgttgtcc aggatggaat tactctgatc2220  
 accaaagagg aagcctcttg aagttctgtc acagctgagg aagccaaaaa gtttctggcc2280  
 cccaaagaca aaccaagtgg agacacagca cgtgtatttg aagaaggtgg tgatgtggac2340  
 gatttatttg acatgatata ggtcgtggat gtatggggaa tctaagagag ctgccatcgc2400  
 tgtgatgctg ggagttctaa caaaacaagt tggatgcggc cattcaaggg gagccaaaat2460  
 ctcaagaaat tcccagcagg ttacctggag gcggtatc atattctctg tggaatgaat2520  
 acacacatat atattacaag ggataattta gacccatac aagtttataa agagtcattg2580  
 ttattttctg gttggtgtat tatttttct gtggtcttac tgatctttgt atattacata2640  
 catgctttga agtttctgga aagtagatct ttcttggacc tagtatatca gtgacagttg2700  
 cagcccttgt gatgtgatta gtgtctcatg tggaaacctg gcatggttat tgatgagttt2760  
 cttaacctt tccagagtc tcttctgct gatcctcaa cagctgtcac aacttgtgtt2820  
 gagcaagcag tagcatttgc ttctctccaa caagcagctg ggttaggaaa accatgggta2880  
 aggacggact cacttctct tttagttgag gccttctagt taccacatta ctctgctct2940  
 gtatataggt ggttttcttt aagtgggtg ggaaggggag cacaatttcc ctctactact3000  
 cttttaagca gtgagttatg gtggtgtct catgaagaaa agaccttttg gcccaatctc3060  
 tgccatatca gtgaaccttt agaaactcaa aaactgagaa atttactaca gtagttagaa3120  
 ttatatcact tcaactgtct ctacttgcaa gctcaaaga gagaaagttt cggtatatta3180  
 aaacacttag gtaacttttc ggtctttccc atttctacct aagtcagctt tcatctttgt3240  
 ggatggtgtc tcttttacta aataagaaaa taacaaagcc cttattctct tttttcttgg3300  
 tctctattct tgccttgagt tccagttcct ctttgggtga cagacttctt ggtaccaggt3360  
 cacctctgtc ttcagcacc tcataagtcg tcaactaatac acagttttgt acatgtaaca3420  
 ttaaaggcat aaatgactca aaaaaaaaaa aaaaaaaaaa aa 3462

## (2) INFORMATION ON SEQ ID NO. 85:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

```

atagggccgg tgctgcctgc ggaagccggc ggctgagagg cagcgaactc atctttgcca 60
gtacaggagc tcgtgccgtg gcccacagcc cacagcccac agccatgggc tgggacctga120
cgggtgaagat gctggcgggc aacgaattcc aggtgtccct gagcagctcc atgtcgggtg180
cagagctgaa ggccgagatc acccagaaga tcggcgtgca cgccttcag cagcgtctgg240
ctgtccaccc gagcgggtgt ggcctgcagg acaggggtccc ccttgccagc cagggcctgg300
gccccggcag cacggtcctg ctggtggtgg acaaatgcga cgaacctctg agcatcctgg360
tgaggaataa caagggccgc agcagcacct acgaggtgcg gctgaacgag accgtggccc420
acctgaagca gcaagtgagc gggctggagg gtgtgcagga cgacctgttc tggctgacct480
tcgaggggaa gcccctggag gaccagctcc cgctggggga gtacggcctc aagcccctga540
gcacogtgtt catgaatctg cgcctgcggg gaggcggcac agagcctggc gggcggagct600
aagggcctcc accagcatcc gagcaggatc aagggccgga aataaaggct gttgtaaaga660
gaaaaaaaa

```

668

## (2) INFORMATION ON SEQ ID NO. 86:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 671 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

```

ggaaaccggt ctcattgaac tcgcctgcag ctcttgggtt ttttgtgget tccttcgtta 60
ttggagccag gcctacaccc cagcaaccat gtccaaggga cctgcagttg gtattgatct120
tggcaccacc tactcttctg tgggtgtttt ccagcacgga aaagtcgaga taattgccaal80
tgatcaggga aaccgaacca ctccaagcta tgcgcctttt acggacactg aacggttgat240
cgggtgatgcc gcaaagaatc aagttgcaat gaaccccacc aacacagttt ttgatgcca300
acgtctgatt ggacgcagat ttgatgatgc tggtgtccag tctgatatga aacattggcc360
ctttatgggtg gtgaatgatg ctggcaggcc caaggtccaa gtagaataca agggagagac420
caaaagcttc tatccagagg aggtgtcttc tatggttctg acaaagatga aggaaattgc480
agaagcctac cttgggaaga ctgttaccac tgcttgtggt cacagtgcc gcttacttta540
atgactctca gcgtcaggct accaaaagat gctggagact attgatggc tgcaatgtac600
tttaggaatt atttaattga gccaaacttg tgccctggtaa tttctttacg ggtttgggca660
aaaaaagggt t                                     671

```

## (2) INFORMATION ON SEQ ID NO. 88:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1108 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

```

agtggaggag ggagagacgc tggcccgga cccgaggggc gtgggcatcg ggaggcgggc 60
ccgggttagg ggcgggaccg ccgcctggtt aaaggcgctt atttcccagg cagccgctgc 120
agtcgccaca cctttgcccc tgcctgcatg accctgtcgc cacttctgct tcggacgtcc 180
ccacggcggc ggtgcaggcg tcccctctgc aagcgtaga cttctttggg aatgggccac 240
cagttaacta caagacaggc aatctatacc tgcggggggc cctgaagaag tccaatgcac 300
cgcttggtcaa tgtgacctc tactatgaag cactgtgcgg tggctgccga gccttcctga 360
tcggggagct cttcccaaca tggctgttg tcatggagat cctcaatgtc acgctggtgc 420
cctacggaaa cgcacaggaa caaatgtca gtggcagggt ggagttcaag tgccagcatg 480
gagaagagga gtgcaaattc aacaagggtg aggcctgcgt gttggatgaa cttgacatgg 540
agctagcctt cctgaccatt gtctgcatgg aagagtttga ggacatggag agaagtctgc 600
cactatgcct gcagctctac gcccagggc tgcgccaga cactatcatg gagtgtgcaa 660
tgggggaccg cggcatgcag ctcatgcacg ccaacgcccc gcggacagat gctctccagc 720
caccgcacga gtatgtgcc tgggtcaccg tcaatgggaa acccttggaa gatcagaccc 780
agctccttac ccttgtctgc cagttgtacc agggcaagaa gccggatgtc tgcccttcct 840

caaccagctc cctcaggagt gtttgcttca agtgcaggcc ggtgagctgc ggagagctca 900
tggaaggcga gtgggaaccc ggctgcctgc cttttttct gatccagacc ctccgcacct 960
gctacttacc aactggaaaa ttttatgcat cccatgaagc ccagatacac aaattccac1020
cccatgatca agaactctgc tccactaaga atgggtgctaa agtaaaacta gtttaataag1080
ccccaaaaaa aaaaccgcgt cggtcgac 1108

```

## (2) INFORMATION ON SEQ ID NO. 89:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

```

aaagcagccg ccggcgccgg gtgcctcaca gcacgctgcc acgcccagcg agaccctct 60
ctgcacgcca gcccgcccgc acccaccatg gccacagttc agcagctgga aggaagatgg120
cgcttggtgg acagcaaagg ctttgatgaa tacatgaagg agctaggagt gggaatagct180
ttgcgaaaaa tgggcgcaat ggccaagcca gattgtatca tcacttgtga tggtaaaaac240
ctcaccataa aaactgagag cactttgaaa acaacacagt tttctgtac cctgggagag300
aaagtttgaag aaaccacagc tgatggcaga aaaactcaga ctgtctgcaa ctttacagat360
ggtgcattgg ttcagcatca ggagtgggat ggggaaggaaa gcacaataac aagaaaattg420
aaagatggga aattagtggg ggagtgtgtc atgaacaatg tcacctgtac tcggatctat480
gaaaaagtag aataaaaatt ccatcatcac tttggacagg agttaattaa gagaatgacc540
aagctcagtt caatgagcaa atctccatc tgcttcttct tttttttttt cattactgtg600
ttcaattatc tttatcataa acattttaca tgcagctatt tcaaagtgtg ttggattaat660
taggatcatc cctttggtta ataaataaat gtgtttgtgc taaaaaaaaa aaaaaaaaaa720

```

## (2) INFORMATION ON SEQ ID NO. 90:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 837 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

ctctgcgag gattggctgt tagcggcgtt gtagttaagc tcgtgtaacg gggcggtgt 60
cggcagctgc ttagcggaag agagtttggc gcatgtctc acaccatttt gctggtagag120
cctaccaaga ggccagaagg cagaacttat gctgactacg aatctgtgaa tgaatgcatg180
gaaggtgttt gtaaaatgta tgaagaacat ctgaaaagaa tgaatcccaa cagtcctct240
atcacatatg acatcagtcg gttgtttgat ttcacgatg atctggcaga cctcagctgc300
ctggtttacc gagctgatac ccagacatac cagccttata acaaagactg gattaaagag360
aagatctacg tgctccttcg tcggcaggcc caacaggctg ggaaataatt gtgttggaag420
cactgggggg gttggggtgg gcttggaaca caggtgtgta cagcgtgctg tagtggaagt480
tttgtatcat agtaatcctg tttccacttt gttatactct agccaagatt gactgtatta540
gatgaaatgt gaggatcctg ttcaatcgga aacccccgtt acctcctctt tttcttctc600
tttctttttt tttttttact taaacatttt tatgatgatt tagatggaag ttgtctctcg660
tcacttaatg ttggttccag tccttcaact gttcatatct actttataac attcacatac720
taacccctct tcaagatggg gtggggggtg gaaatgcagt ttagccatgt cctcaagata780
aagtccttgg aaaaataaat aaatgtcctt tagttataaa aaaaaaaaaa aaaaaaa 837

```

## (2) INFORMATION ON SEQ ID NO. 91:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 498 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

gtagggtcag cgtcggaggc ggtagtgcag gtggcggttc cttgaggaag agtgagggtt 60
ccaaacttttc tgcttatctg ggaggtgttg ggcgcggaaca gtcgagatgt cagagaaaaa120
gcagccggta gacttaggtc tgtagagga agacgacgag tttgaagagt tccctgccga180
agactgggct ggcttagatg aagatgaaga tgcacatgtc tgggaggata attgggatga240
tgacaatgta gaggatgact tctcaatca gttacgagct gaactagaga aacatgggta300
taagatggag acttcatagc atccagaaga agtggtgaag taacctaaac ttgacctgct360
taatacattc tagggcagag aacccaggat gggacactaa aaaaatgtgt ttatttcatt420
atctgcttgg atttatttgt gtttttgtaa cacaaaaaat aaatgttttg atataaaaag480
gaaagagaaa aattgcgg                                     498

```

(2) INFORMATION ON SEQ ID NO. 92:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1077 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:



(vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cggctcgagc tggtaacaaca gggcacacgt gtttcacggt gacaggtttg cttgggacgc 60
tagtaaccat gggcttgctg acttagccaa agaagagtta agaagaaaat acacacaagt 120
atacagactg ttctagttt cttagactta tctgcatatt ggataaaaata aatgcaattg 180
tgctcttcat ttaggatgct ttcatgtct ttaagatgtg ttaggaatgt caacagagca 240
aggagaaaaa aggcagtcct ggaatcacat tcttagcaca cctacacctc ttgaaaatag 300
aacaacttgc agaattgaga gtgattcctt tcctaaaagt gtaagaaaagc atagagattt 360
gttcgtattt agaattggat caccaggaaa agagaaggaa agtgattttt ttccacaaga 420
tctgtaattg tatttccact tataaaggaa ataaaaaatg aaaaacatta tttggatatt 480
aaaagcaaat aaaaacccaa ttcagtctct tctaagcaaa attgctaaag agagatgaac 540
cacattataa agtaatcttt ggctgtaagg cattttcatc ttctcttcgg gttggcaaaa 600
tattttaaag gtaaaacatg ctggtgaacc aggggtgttg atggtgataa gggaggaata 660
tagaatgaaa gactgaatct tctttgttg cacaatatga gtttgaaaaa agcctgtgaa 720
aggtgtcttc ttgacttaa tgtctttaa agtatccaga gatactacaa tattaacata 780
agaaaagatt atatattatt tctgaatcga gatgtccata gtcaaatttg taaatcttat 840
tcttttgtaa tatttattta tatttattta tgacagttaa cattctgatt ttacatgtaa 900
aacaagaaaa gttgaagaag atatgtgaag aaaaatgtat ttttctaaa tagaaataaa 960
tgatcccatt ttttggtaaa aaaaagtatg tgagatttat tcgtaaacgt gactactttal1020
tttctaaata agagattccc tacctgcgtc ctacaagcag ttcagaatgc catgcct 1077

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1755 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

cgcagggtctg cttgtgatct ggtacgagga ttatgcaagt tttttgaggg acctgtgaca 60
ggaatcttct ctggttatgt taattccatg ctgcaggaat acgcaaaaaa tccatctgtc 120
aactggaaac acaaagatgc agccatctac ctagtgcacat ctttggcatc aaaagcccaa 180
acacagaagc atggaattac acaagcaaat gaacttgtaa acctaactga gttctttgtg 240
aatcacatcc tccctgattt aaaatcagct aatgtgaatg aatttcctgt ccttaaagct 300
gacggtatca aatatattat gatttttaga aatcaagtgc caaaagaaca tcttttagtc 360
tcgattcctc tcttgattaa tcattctcaa gctgaaagta ttgttggtca tacttacgca 420
gctcatgctc ttgaacggct ctttactatg cgagggccta acaatgccac tctctttaca 480
gctgcagaaa tcgcaccgtt tgttgagatt ctgctaacaa accttttcaa agctctcaca 540
cttcctggct cttcagaaaa tgaatatatt atgaaagcta tcatgagaag tttttctctc 600
ctacaagaag ccataatccc ctacatccct actctcatca ctcagcttac acagaagcta 660
ttagctgtta gtaagaacct aagcaaacct cactttaatc actacatgtt tgaagcaata 720
tgtttatcca taagaataac ttgcaaagct aaccctgctg ctggttgtaa ttttgaggag 780
gctttgtttt tgggtgtttac tgaaatctta caaaatgatg tgcaagaatt tattccatac 840
gtctttcaag tgatgtcttt gcttctggaa acacacaaaa atgacatccc gtcttcttat 900
atggccttat ttctcatct ccttcagcca gtgctttggg aaagaacagg aaatattcct 960
gctctagtga ggcttcttca agcattctta gaacgcggtt caaacacaat agcaagtgtc1020
gcagctgaca aaattcctgg gttactaggt gtctttcaga agctgattgc atccaaagca1080
aatgaccacc aagggttttta tcttctaaac agtataatag agcacatgcc tctgaatca1140
gttgaccaat ataggaaaca aatcttcatt ctgctattcc agagacttca gaattccaaa1200
acaaccaagt ttatcaagag ttttttagtc tttattaatt tgtattgcat aaaatatggg1260
gcactagcac tacaagaaat atttgatggt atacaaccaa aaatgtttgg aatggttttg1320
gaaaaaatta ttattcctga aattcagaag gtatctggaa atgtagagaa aaagatctgt1380
gcggttgcca taaccaaatt actaacagaa tgtcccccac tgatggacac tgagtatacc1440
aaactgtgga ctccattatt acagtctttg attgggtctt ttgagttacc cgaagatgat1500
accattcctg atgaggaaca ttttattgac atagaagata caccaggata tcagactgcc1560
ttctcacagt tggcatttgc tgggaaaaaa gagcatgac ctgtaggtca aatggtgaat1620
aaccacaaaa ttcacctggc acagtcaact cacaagttgt ctaccgctg tccaggaagg1680
gttccatcaa tggcaaagaa ctctgtgata aatggagact ttaatgggag ggcaaaagg1740
tagtagtagt tctgg                                     1755

```

## (2) INFORMATION ON SEQ ID NO. 94:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

gttcggcgag cgagcacctt cgacgcggtc cggggacccc tegtgcgtgt cctcccgacg 60
cggacccggg gccccaggct cgcgctgccc ggcagggtgc tegtgtccca ctcccgggcg 120
acgcctcccg cgagtcctcg gccctcccg cgcctctctt ctggcgcgcg gcgcagatgg 180
gcgcccccg aggtcctcgc gttcgggctt ctgcttgccg cggcgacggc gacttttgcc 240
gcagctcagg aagaatgtgt ctgtgaaaac tacaagctgg ccgtaaactg ctttgtgaat 300
aataatcgtc aatgccagtg tacttcagtt ggtgcacaaa atactgtcat ttgctcaaag 360
ctggctgcca aatgttttgt gatgaaggca gaaatgaatg gctcaaaact tgggagaaga 420
gcaaaacctg aaggggccct ccagaacaat gatgggcttt atgatcctga ctgcgatgag 480
agcgggctct ttaaggccaa gcagtgcac ggcacctcca tgtctgggtg tgtgaacact 540
gctgggggtca gaagaacaga caaggacact gaaataacct gctctgagcg agtgagaacc 600
tactggatca tcattgaact aaaacacaaa gcaagagaaa aaccttatga tagtaaaagt 660
ttgcggactg cacttcagaa ggagatcaca acgcgttatc aactggatcc aaaatttacc 720
acgagtattt tgtatgagaa taatgttatc actattgatc tggttcaaaa ttcttctcaa 780
aaaactcaga atgatgtgga catagctgat gtggcttatt attttgaaaa agatgttaaa 840
ggtgaatcct tgtttcattc taagaaaatg gacctgacag taaatgggga acaactggat 900
ctggatcctg gtcaaaacttt aatttattat gttgatgaaa aagcacctga attctcaatg 960
cagggctctaa aagctgggtg tattgctggtt attgtggttg tggatagac agttgtgct1020
ggaattgttg tgctggttat ttccagaaaag aagagaatgg caaagtatga gaaggctgag1080
ataaaggaga tgggtgagat gcatagggaa ctcaatgcat aactatataa tttgaagatt1140
atagaagaag ggaaatagca aatggacaca aattacaaat gtgtgtgcgt gggacgaag1200
catctttgaa ggtcatgagt ttgttagttt aacatcatat atttgaata gtgaaacctg1260
tactcaaaat ataagcagct tgaactggc tttaccaatc ttgaaatttg accacaagt1320
tcttatatat gcagatctaa tgtaaaatcc agaacttggc ctccatcggt aaaattatt1380
atgtgtaaca ttcaaatgtg tgcattaaat atgcttcac agtaaaatct gaaaaactga1440
tttgtgattg aaagctgcct ttctatttac ttgagtcttg tacatacata cttttttatg1500
agctatgaaa taaaacattt taaactgaaa aaaaaaaaaa aaggc 1545

```

## (2) INFORMATION ON SEQ ID NO. 95:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1133 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

gcgcgggtatt atcgggtaga catctcgac cgcgtctcgg aaaccggtag cgcttgcagc 60
atggctgacc aactgactga agagcagatt gcagaattca aagaagctt ttactattt 120
gacaaagatg gtgatggaac tataacaaca aaggaattgg gaactgtaat gagatctctt 180
gggcagaatc ccacagaagc agagttagag gacatgatta atgaagtaga tgctgatggt 240
aatggcacia ttgaacttcc ctgaatttct ggacaaggat ggcaagaaaa atgaaagaca 300
cagacagtga agaagaaatg agagaagcat tccgtgtgtt tgataaggat ggcaagggct 360
atatgagtgc tgcagaactt cgccatgtga tgacaaacct tggagagaag ttaacagatg 420
aagaagttga tgaatgatc agggaaagcag atattgatgg tgatggtaa gtaaaactatg 480
aagagtttgt acaaatgatg acagcaaatg gaagaccttg tacagaatgt gttaaatttc 540
ttgtacaaaa ttgtttattt gccttttctt tgtttgtaac ttatctgtaa aagggtttctc 600
octactgtca aaaaaatatg catgtatagt aattaggact tcattcctcc atgttttctt 660
cccttatctt actgtcattg tcctaaaacc ttattttaga aaagttgatc aaggtaacat 720
gttgcatgtg gcttactctg gggaaatatc taagcccttc tgcacatcta aacttagatg 780
gagttggcca aatgagggaa catctgggtt atgccttttt taaagtagtt ttcttttagga 840
actgtcagca tgttggtgtt gaagtgtgga gttgtaactc tgcgtggact atggacagtc 900
aacaatatgt acttaaaagt tgcactattg caaaacgggt gtattatcca ggtactcgta 960
cactattttt ttgtactgct ggtcctgtac cagaaacatt ttcttttatt gttacttgct 1020
ttttaaactt ggttttagcca cttaaaatct gcttatggca caatttgccc caaaatccat 1080
tccaagttgt atatttgttt tccaataaaa aaattacaat ttacccaaaa aaa 1133

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 791 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:**

```

gccgcccgcg cggaccgggc gagaggcggc ggcgggagcg gcggtgatgg acgggtccgg 60
ggagcagccc agaggcgggg ggcccaccag ctctgagcag atcatgaaga caggggccct120
tttgcttcag ggtttcatcc aggatcgagc agggcgaaatg gggggggagg caccgagct180
ggccctggac ccggtgcctc aggatgcgtc caccaagaag ctgagcgagt gtctcaagcg240
catcggggac gaactggaca gtaacatgga gctgcagagg atgattgccg ccgtggacac300
agactcccc cgagaggtct tttccgagt ggcagctgac atgtttctg acggcaactt360
caactggggc cgggttgctg cccttttcta ctttgccagc aaactgggtg tcaaggccct420
gtgcaccaag gtgccggaac tgatcagaac catcatgggc tggacattgg acttcctccg480
ggagcggctg ttgggctgga tccaagacca ggggtggttg gacggcctcc tctcctactt540
tgggacgccc acgtggcaga ccgtgaccat ctttggtggc ggagtgtca ccgcctcact600
caccatctgg aagaagatgg gctgaggccc ccagctgcct tggactgtgt ttttctcca660
taaatattgg catttttctg ggaggggtgg ggattggggg acatgggcat ttttcttact720
tttgtaatta ttgggggggtg tggggaagag tggctctgag ggggtaataa acctccttcg780
ggacacaaaa a

```

791

**(2) INFORMATION ON SEQ ID NO. 97:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 599 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing

**(iii) HYPOTHETICAL:** NO

**(iii) ANTI-SENSE:** NO

**(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

**(vii) OTHER ORIGIN:**

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:**

```

tcttgcttc accatgaagt ccagcggcct ctcccccttc ctggtgctgc ttgccctggg 60
aactctggca ccttgggctg tgggaaggctc tggaaagtcc ttcaaagctg gagtctgtcc120

tccaaagaaa tctgcccagt gccttagata caagaaacct gagtgcaga gtgactggca180
gtgtccaggg aagaagagat gttgtcctga cacttgaggc atcaaagtcc tggatcctgt240
tgacacccca aacccaacaa ggaggaagcc tgggaagtgc ccagtgaact atggccaatg300
tttgatgctt aaccccccca atttctgtga gatggatggc cagtgcagc gtgacttgaa360
gtgttgcatg ggcattgtgt ggaaatcctg cgtttccctt gtgaaagctt gattcctgcc420
atatggagga ggcctctggg tctgtctctg tgtgggtccag gtcctttcca ccttgagact480
tggtccacc actgatatcc tcttttgggg aaaggccttg cacacagcag gctttcaaga540
agtgccagtt gatcaatgaa taataaaacg agcctatttc tctttgcaaa aaaaaaaaa 599

```

**(2) INFORMATION ON SEQ ID NO. 98:**

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 643 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

gggcccgcgg ctcggggcgta ggaggcgggtg cctctgcagc aagcgtgggg cgcggaacc 60
cgagcaggac tctccagtc tccagtcacct tggacaaaga agtgtggatc ctcagattcc120
atctttttcca actccaaggt gccatggcag agaagggtgct ggtaacaggt ggggctggct180
acattggcag ccacacgggtg ctggagctgc tggagggtg ctacttgctt gtggtcatcg240
ataacttcca taatgccttc cgtggagggg gctccctgcc tgagagcctg cggcgggtcc300
aggagctgac aggcgcgtct gtggagtttg aggagatgga cattttggac cagggaagccc360
tacagcgtct cttcaaaaag tacagcttta tggcgggtcat ccactttgcg gggctcaagg420
ccgtggggcga gtcgggtgcag aagcctctgg attattacag agttaacctg accgggacca480
tccagcttct ggagatcatg aaggccacg ggggtgaagaa cctgggtgttc agcagctcag540
ccactgtgta cgggaacccc cagtacctgc ccccttgaat gagggccacc ccacggggtg600
ggatgtaaca accttacgga agtccaaatt tctttatctt ttc 643

```

## (2) INFORMATION ON SEQ ID NO. 99:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 860 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

ctcgagccgc tcgagccgat tcggctcgag tgccctccaga ggactggcca ctttttgcc 60
agataaagat gcacttagag atgaatatga tgatctctca gatttgaatg cagtacaaat120
ggagagtgtt cgagaatggg aaatgcagtt taaagaaaaa tatgattatg taggcagact180
cctaaaacca ggagaagaac catcagaata tacagatgaa gaagatacca aggatcacaa240
taaacaggat tgaactttgt aaacaaccaa agtcaggggc cttcagaact gcaattctta300
ctccctttca cagactgtcc ggagtctttg ggtttgattc aocctgctgcg aaaaacattc360
aacaaattgt gtacaagata aattaatctc actatgaaga tttgaataac tagacattat420
ttatgctgcc aaactcattt gttgcagttg tttgtaatgt ctagtggggc ttcattcatcc480
tgaaaagaag gagacaggga tttttttaa gagcaagaaa gtcacaatat tacttctttc540
cttctttttt tcttctttt ctttctttt tcttctttt tcttttttaa atatttgaa600
gacaaccaga tatgtatttg ctactcaagt gtacagatct cctcaagaaa catcaaggga660
ctcctgtgtc acatactgtg tttttatttt aacatgggtg agggaggcga cctgatcagg720
ggaggtgggg gtacacatca atttgagttg ttcaggctac tgaaacatta aaatgtgaat780
tcccaaactt ttcttttttg cattgttcgg gggataggga aatatcggtt ttaaaggagt840
cttggaatt gggtgtggga
860

```

## (2) INFORMATION ON SEQ ID NO. 100:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

cggggctggc ccagcctggg ccgggggagag gactgggtgg gcagggggogc cgccccgcct 60
cgggagagggc gggccggggc gggctggggag tatttgaggg tcggagccac cgccccgcgg 120
ggccccgcag caccctcctcg ccagcagccg tccggagcca gccaacgagc ggaaaatggc 180
agacaatttt tcgctccatg atgcgttatc tgggtctgga aacccaaacc ctcaaggatg 240
gcctggcgca tgggggaacc agcctgctgg ggcagggggc taccaggggg ctccctatcc 300
tggggcctac cccgggcagg caccgccagg ggcttatcct ggacaggcac ctccaggcgc 360
ctaccctgga gcacctggag cttatcccg agcacctgca cctggagtct acccagggcc 420
accagcgggc cctggggcct acccatcttc tggacagcca agtgccaccg gaggctaccc 480
tgccactggc cctatggcg cccctgctgg gccactgatt gtgccttata acctgccttt 540
gcctggggga gtggtgcctc gcatgctgat aacaattctg ggcacggtga agcccaatgc 600
aaacagaatt gctttagatt tccaaagagg gaatgatgtt gccttccact ttaaccacg 660
cttcaatgag aacaacagga gagtcattgt ttgcaatata aagctggata ataactgggg 720
aagggaagaa agacagtcgg ttttccatt tgaaagtggg aaaccattca aaatacaagt 780
actggttgaa cctgaccact tcaaggttgc agtgaatgat gctcacttgt tgcagtacaa 840
tcctcggtt aaaaaactca atgaaatcag caaactggga atttctggtg acatagacct 900
caccagtgtc tcataatacca tgatataatc tgaaaggggc agattaaaaa aaaaaaaaaga 960
atctaaacct tacatgtgta aaggtttcat gttcactgtg agtgaaaatt ttacattcal1020
tcaatatccc tcttgtaagt catctactta ataaatatta cagtgaaaaa aaaaaaaaaa1080
aaaaaaaaaa gtcgaaaaag gagggggaag gagagagagg gaagaagaga gaggagaagg1140
aggggggggg tgggt                                     1155

```

## (2) INFORMATION ON SEQ ID NO. 101:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 522 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aaaaatatct gctggaaatt gctgtgtagg attacaggcg tgaccactgc gcccgggccac 60
attcagttct tatcaaagaa ataaccgaga cttaattctg aatgatacga ttatgcccaal20
tattaagtaa aaaatataag aaaagggttat cttaaataga tcttaggcaa aataccagct180
gatgaaggca tctgatgcct tcactgttcc agtcatctcc aaaaacagta aaaataacca240
ctttttgttg ggcaatatga aattttttaa ggagtagaat accaaatgat agaaacagac300
tgctgaatt gagaattttg atttcttaaa gtgtgtttct ttctaaattg ctgttcctta360

```



```

atttgattaa ttttaattcat gtattatgat taaatctgag gcagatgagc ttacaagtat420
tgaaataatt actaattaat cacaaatgtg aagttatgca tgatgtaaaa aatacaaaaca480
ttctaattaa aggctttgca acacaaaaaa aagaaaaaaa aa 522

```

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1628 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ccagctcgcc ctgcctagcc agggggcgccc cgccccctgc ctgcccggcc accttcggga 60
gccgcttcca ataggcgcttc gccattggct ctggcgacct ccgcgcgttg ggaggtgtag 120
cgcggtctctg aacgcgctga gggccggttga gtgtcgacag cgcgaggggc gcgagttagg 180
agcagaccca ggcacgcgcg gccgagaagg ccgggcgtcc ccacactgaa ggcccgaaa 240
ggcgacttcc gggggctttg gcacctggcg gacctcccgc gagcgctggc acctgaacgc 300
gagcgctcc attgcgcgtg cgcgttgagg ggcttcccgc acctgatcgc gagaccccaa 360
cggctggttg cgtcgccctgc gcgtctcgcc tgaagtgccc atggcgagc gtgcgggctg 420
aggcggagcg ggcgtttctc gccctgcttg gatcgctgct cctctctggg gtcctggcgg 480
ccgaccgaga acgcagcatc cacgacttct gcctggtgtc gaaggtggtg gccagatgcc 540
gggcctccat gcctaggttg tggtagaatg tctactgacg atcctgccag ctgtttgtgt 600
atgggggctg tgacggaaac agcaataatt acctgaccaa ggaggagtgc ctcaagaaat 660
gtgccactgt cacagagaat gccacgggtg acctggccac cagcaggaat gcagcggtt 720
cctctgtccc aagtgtctcc agaaggcagg attctgaaga cactccagc gatatgttca 780
actatgaaga atactgcacc gccaacgcag tcaactggcc ttgccgtgca tccctccac 840
gctggtactt tgacgtggag aggaactcct gcaataactt catctatgga ggctgccggg 900
gcaataagaa cagctaccgc tctgaggagg cctgcatgct ccgctgcttc cgccagcagg 960
agaatcctcc cctgcccctt ggcctcaaagg tgggtggtct ggccgggctg ttcgtgatgg 1020
tggtgatcct ctctcctggga gcctccatgg tctacctgat ccgggtggca cggaggaacc 1080
aggagcgtgc cctgcgaccc gtctggagct ccggagatga caaggagcag ctggtgaagall 1140
acacatatgt cctgtgaccg ccctgtcgcc aagaggactg gggaagggag gggagactat 1200
gtgtgagctt tttttaaata gagggattga ctcgatttg agtgatcatt agggctgagg 1260
tctgtttctc tgggaggtag gacggctgct tctgtgtctg gcagggatgg gtttgccttg 1320
gaaatcctct aggaggctcc tctctgcatt gcctgcagtc tggcagcagc cccgagttgt 1380
ttcctcgctg atcgatttct ttctccagg tagagtttct tttgcttatg ttgaattcca 1440
ttgcctcttt tctcatcaca gaagtgatgt tggaaatcgt tcttttggtt gctgatttal 1500
tggttttttt aagtataaac aaaagttttt tattagcatt ctgaaagaag gaaagtaaaa 1560
tgtacaagtt taataaaaaa gggccttccc cttagaata aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaa 1628

```

## (2) INFORMATION ON SEQ ID NO. 103:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 605 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

cctggcagct gtcggctgga aggaactggt ctgctcacac ttgctggctt gcgcatcagg 60
actggcttta tctcctgact cacggtgcaa aggtgcactc tgcgaacggt aagtccgtcc120
ccagcgcttg gaatcctacg gccccacag ccggatcccc tcagccttcc aggtcctcaa180
ctcccccgga cgctgaacaa tggcctccat ggggctacag gtaatgggca tcgcgctggc240
cgtcctgggc tggctggccg tcatgctgtg ctgcgcgtg cccatgtggc gcgtgacggc300
cttcctcggc agcaacattg tcacctcgca gaccatctgg gagggcctat ggatgaactg360
cgtggtgcag agcaccggcc agatgcagtg caagggtgtac gactcgctgc tggcactgcc420
gcaggacctg caggcggccc gcgccctcgt catcatcagc atcatcgtgg ctgctctggg480
cgtgctgctg tccgtggtgg ggggcgaagt gtaacaaact tgcctggagg attaaaagcg540
ccaagggcaa gaacatgatt cgttggcggg cgtgggtgtt tctgtttggg ccggccta600
gggtg                                         605

```

## (2) INFORMATION ON SEQ ID NO. 105:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2731 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agggggggcg acagacacag actatgcaga tgggagtgaa gacaaagtag tagaagtagc 60
agaggaggaa gaagtggctg aggtggagga cgatgaggat ggtgatgagg tagaggaaga 120
ggctgaggaa ccctacgaag aagccacaga gagacacaga gtctgtggaa gaggtggttc 180
gagaggtgtg ctctgaacaa gccgagacgg ggccgtgccg agcaatgac tcccgttgtt 240
actttgatgt gactgaaggg aagtgtgccc cattctttta cggcggatgt gccggcaacc 300
ggaacaactt tgacacagaa gactactgca tggccgtgtg tggcagcgcc attcctacaa 360
cagcagccag taccctgat gccgttgaca agtatctcga gacacctggg gatgagaatg 420
aacatgcccc tttccagaaa gccaaagaga ggcttgaggc caagcaccga gagagaatgt 480
cccaggtcat gagagaatgg gaagaggcag aacgtcaagc aaagaacttg cctaaagctg 540
ataagaaggc agttatccag catttccagg aaaaagtgga atctttggaa caggaagcag 600
ccaacgagag acagcagctg gtggagacac acatggccag agtggaaagg atgctcaatg 660
accgcccggc cctggccctg gagaactaca tcaccgtctc gcaggctgtt cctcctcggc 720
ctcgtcacgt gttcaatatg ctaaagaagt atgtccgcgc agaacagaag gacagacaga 780
acaccctaaa gcatttctgag catgtgcgca tgggtgatcc caagaaagcc gctcagatcc 840
ggcccagggt tatgacacac ctccgtgtga tttatgagcg catgaatcag tctctctccc 900
tgctctacaa cgtgcttgca gtggccgagg agattcagga tgaagtgtat gagctgcttc 960
agaaagagca aaactattca gatgacgtct tggccaacat gattagttaa ccaaggatca 1020
gttacggaaa cgatgctctc atgccatctt tgaccgaaac gaaaaccacc gtggagctcc 1080
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agtacacatc cattcatcat ggtgtggtgg aggttgacgc cgctgtcacc ccagaggagc 1500
gccacctgtc caagatgcag cagaacggct acgaaaatcc aacctacaag ttctttgagc 1560
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tcactaccca tcggtgtcca tttatagaat aatgtgggaa gaaacaaacc cgttttatga 1680
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ttaatccaca catcagtaat gtattctatc tctctttaca ttttggctc tatactacat 1800
tattaatggg ttttgtgtac tgtaaagaat ttagctgtat caaactagtg catgaataga 1860
ttctctcctg attattttat acatagcccc ttagccagtt gtatattatt cttgtggttt 1920
gtgacccaat taagtccctac tttacatatg ctttaagaat cgatggggga tgcttcattg 1980
gaacgtggga gttcagctgc ttctcttgcc taagtattcc tttcctgatc actatgcatt 2040
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cattttactg tacagattgc tgcttctgct atattttgtg tataggaatt aagaggatac 2160
acacgtttgt ttcttcgtgc ctgttttatg tgacacacatt aggcattgag acttcaagct 2220
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taagcacttt tacggggcgg gtggggaggg gtgctctgct ggtcttcaat taccaagaat 2340
tctccaaaac aattttctgc aggatgattg tacagaatca ttgcttatga catgatcgct 2400
ttctacactg tattacataa ataaattaaa taaaataacc ccgggcaaga cttttctttg 2460
aaggatgact acagacatta aataatcgaa gtaatttttg gtggggagaa gaggcagatt 2520
caattttctt taaccagctc gaagtttcat ttatgatata aaagaagatg aaaaatgga 2580
tgccaatata aggggatgag gaaggcatgc ctggacaaac cttcttttta agatgtgtct 2640
tcaatttgta taaaatgggt ttttcatgta aataaatata ttcttgagg agccaaaaaa 2700
aactatatta ctggcaggtt tataatatgg c
2731

```

## (2) INFORMATION ON SEQ ID NO. 106:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2194 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

gaattcagaa gttaatgatg ttgggtaaga gaacaatggt aagagagcaa tctaagaata 60
tatcacctac ttttaatttta tatgagagta catggaggta gctgtgatgt ggaaatgtag 120
cactgctcct acccacgcag atttattcca gtgaaacaac aactggaact tcaagtaact 180
cctcccagag taattccaac tctgggttgg ccccaaatcc aactaatgcc accaccaagg 240
cggctgtgtg tgccctgcag tcaacagcca gtctcttcgt ggtctcactc tctctctgc 300
atctctactc ttaagagact caggccaaga aacgtcttct aaatttcccc atctctctaaa 360
cccaatccaa atggcgtctg gaagtccaat gtggcaagga aaaacaggtc ttcctcgaat 420
ctactaattc cacacctttt attgacacag aaaatgttga gaatcccaa tttgattgat 480
ttgaagaaca tgtgagaggt ttgactagat gatggatgcc aatattaaat ctgctggagt 540
ttcatgtaca agatgaagga gaggcaacat ccaaaatagt taagacatga tttccttgaa 600
tgtggcttga gaaatattga cacttaatac taccttgaaa ataagaatag aaataaagga 660
tgggattgtg gaatggagat tcagttttca tttggttcat taattctata aggccataaa 720
acaggtaata taaaaagctt ccattgattct acatgagaag gaacttccag 780
gtgttactgt aattcctcaa cgtattgttt cgacagcact aatttaatgc cgatatactc 840
tagatgaagt ttacattgt tgagctattg ctgttctctt gggaactgaa ctacttttcc 900
tcttgaggct ttggatttga cattgcattt gaccttttat gtagtaattg acatgtgcca 960
gggcaatgat gaatgagaat ctacccccag atccaagcat cctgagcaac tcttgattat 1020
ccatattgag tcaaattgta ggcattttct atcacctgtt tccattcaac aagagcacta 1080
cattcattta gctaaacgga ttccaaagag tagaattgca ttgaccgcga ctaatttcaal 1140
aatgcttttt attattatta ttttttagac agtctcactt tgtcgcccag gccggagtgc 1200
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tcagcctccc aagtagctgg gattacaggc acctgccacc atgcccggtt aatttttgta 1320
attttagtag agacagggtt tcaccatgtt gccagggtg gtttcgaact cctgacctca 1380
ggtgatccac ccgcctcggc ctcccaaagt gctgggatta caggcttgag ccccgcgcc 1440
cagccatcaa aatgcttttt atttctgcat atgttgaata ctttttaca tttaaaaaaa 1500
tgatctgttt tgaaggcaaa attgcaaata ttgaaattaa gaaggcaaaa atgtaaagga 1560
gtcaaaaacta taaatcaagt atttggaag tgaagactgg aagctaattt gcattaaatt 1620
cacaaacttt tatactcttt ctgtatatac atttttttcc tttaaaaaac aactatggat 1680
cagaatagcc acatttttaga cactttttgt tatcagtgaa tatttttaga tagttagaac 1740
ctggctctaa gcctaaaagt gggcttgatt ctgcagtaaa tcttttaca ctgcctcgac 1800
acacataaac ctttttaaaa atagacactc cccgaagtct tttgttcgca tggtcacaca 1860
ctgatgctta gatgttccag taatctaata tggccacagt agtcttgatg accaaagtcc 1920
tttttttcca tcttttagaaa actacatggg aacaaacaga tcgaacagtt ttgaagctac 1980
tgtgtgtgtg aatgaacact cttgctttat tccagaatgc tgtacatcta ttttgatttg 2040
tatattgtgt ttgtgtattt acgctttgat tcatagtaac ttcttatgga attgatttgc 2100
attgaacaca aactgtaaat aaaaagaaat ggctgaaaga gcaaaaaaaa aggaaagaaa 2160
aaagaaaaaa aaaagaaaaa aaaaaggggg aggc

```

2194

## (2) INFORMATION ON SEQ ID NO. 107:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```

cggaagggtgg accttggatg aattttgacg agaacaagtt cgtggaccga agaagatggg 60
ggccgcacgc ccaggcccg gccccgacga ggccgaggtg gacacctgcc ccctgcgcaa 120
aggaaacatg aaacagaccc tacaggcagc tctgaagaac ccccttatca acaccaagag 180
tcaggcagtg aaggaccggg caggcagcat tgtcttgaag gtgctcatct cttttaaaagc 240
taatgatata gaaaaggcag ttcaatctct ggacaagaat ggtgtggatc tcctaatagaa 300
gtataattat aaaggatttg agagcccgct tgacaatagc agtgctatgt tactgcaatg 360
gcatgaaaag gcacttgctg ctggaggagt aggggccatt gttcgtgtct tgactgcaag 420
aaaaactgtg tagtctggca ggaagtggat tatctgcctc gggagtggga attgctggta 480
aaaagaccaa aacaaccaaa tggcaccgct gcctgtggg tagcatctgt ttctctcagc 540
tttgccttct tgctttttca tatctgtaaa gaaaaaaatt acatatcagt tgccttttaa 600
tgaaaaattg gataatatag aagaaattgt gttaaaaatg aagtgtttca tcttttcaaa 660
accatttcag tgatgtttat accaatctgt atatagtata atttacattc aagttaaatt 720
gtgcaacttt taacccctgt tggctggttt tttgttctgt tttgttttgt attattttta 780
actaatactg agagatttgg tcagaatttg aggccagttt cctagctcat tgctagttag 840
gaaatgatat ttataaaaaa tatgagagac tggcagctat taacattgca aaactggacc 900
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gttcagagca agaagtcttg ctttatacaa atgtatccat aaaatatcag agcttgttgg1140
gcatgaacat caaacttttg ttccactaat atggctctgt ttggaaaaaa ctgcaaatca1200
gaaagaatga tttgcagaaa gaaagaaaaa ctatggtgta atttaaactc tgggcagcct1260
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caactagtat ttaagatacc atttaatatg ccccgtaa at gtcttcagtg ttcttcagggl1380
tagttgggat ctcaaaagat ttggttcaga tccaaacaaa tacacattct gtgttttagc1440
tcagtgtttt ctaaaaaaag aaactgccac acagcaaaaa attgtttact ttgttggaca1500
aaccaaatca gttctcaaaa aatgaccggt gcttataaaa agttataaat atcgagtagc1560
tctaaaacaa accacctgac caagagggaa gtgagcttgt gcttagtatt tacattggat1620
gccagttttg taatcactga cttatgtgca aactggtgca gaaattctat aaactctttg1680
ctgtttttga tacctgcttt ttgtttcatt ttgttttgtt ttgtaaaaat gataaaactt1740
cagaaaataa aatgtcagtg ttgaataaaa taaaaaaca aattgaagaa gaggatggag1800
atttcgactt gg

```

1812

## (2) INFORMATION ON SEQ ID NO. 108:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 890 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

```

aacgactcct ggtaccttgc tcccattact tcccgttttc tggatctgct gctcgtctca 60
ggctcgtagt tcgccttcaa catgcoggaa ccagcgaagt ccgctccgcg gcccaagaag120
ggctcgaaga aagccgtgac taaggcgcag aagaaggacg gcaagaagcg caaggcagcc180
gcaaggagag ctactccgta tacgtgtaca aggtgctgaa gcagggtccac cccgacaccg240
gcatctcctc taaggccatg ggaatcatga actccttcgt caacgacatc ttcgaacgca300
tcgcggtgta ggcttcccg cgtggcgcat acaacaagcg ctcgaccatc acctccagg360
agatccagac ggccgtgcgc ctgctgctgc ccggggagtt ggccaagcac gccgtgtccg420
agggcaccaa ggccgtcacc aagtacacca gcgctaagta aacttgccaa ggagggaact480
tctctggaat ttcctgatat gaccaagaaa gcttcttata aaaagaagca caattgcctt540
cggttacctc attatctact gcagaaaaga agacgagaat gcaaccatac ctatagggac600
ttttccacaa gctaaagctg gcctcttgat ctcatcaga ttccaaagag aatcatttac660
aagttaattt ctgtctcctt ggtccattcc ttctctctaa taatcattta ctgttctca720
aagaattgtc tacattaccc atctcctctt ttgcctctga gaaagagtat ataagcttct780
gtacccactc ggggggttgg ggtaatatc tgtggtcctc agccctgtac cttaataaat840
ttgtatgcct tttctcttaa aaaaaaaaaa aagaagaagg aagaggatgc 890

```

## (2) INFORMATION ON SEQ ID NO. 110:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2627 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

ggcacgagat gtgaaaaggt tttgtgtaca ccacctcaa aaataaaaaa tggaaaacac 60
accttttagtg aagtagaagt atttgagtat ctgtagcag taacttatag ttgtgatcct 120
gcacctggac cagatccatt ttcacttatt ggagagagca cgattttattg tggtgacaat 180
tcagtgtgga gtcgtgctgc tccagagtgt aaagtggta aatgtcgatt tccagtagtc 240
gaaaatggaa aacagatatac aggatttgga aaaaaatttt actacaaagc aacagttatg 300
tttgaatgcg ataagggttt ttacctcgat ggcagcgaca caattgtctg tgacagtaac 360
agtactggg atccccaggt tccaaagtgt cttaaagtgt cgacttcttc cactacaaaa 420
tctccagcgt ccagtgccctc aggtccctag cctacttaca agcctccagt ctcaaatat 480
ccaggatata ctaaacctga ggaaggaata cttgacagtt tggatgtttg ggtcattgct 540
gtgattgtta ttgccatagt tgttggagtt gcagtaattt gtgttgtccc gtacagatat 600
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gatgcttctt tgaaccttgt atgaatttgg gtatgaacag attgcctgct tcccttaaa 900
taacaccttag atttatttga ccagtcagca cagcatgcct ggttgtatta aagcagggat 960
atgctgtatt ttataaaatt ggcaaaatta gagaaatata gttcacaatg aaattatatt 1020
ttctttgtaa agaaagtggc ttgaaatctt tttgttcaa agattaatgc caactcttaa 1080
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gcaattacta agaagcagat aatgggtgtt tttagaaacc taattgaagt atattcaacc 2280
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acatttgatt ttttcaaat taatatttat attagagatc tatatatgta taaatatgta 2400
ttttgtcaaa tttgttactt aaatatatag agaccagttt tctctggaag tttgtttaaa 2460
tgacagaagc gtatatgaat tcaagaaaat ttaagctgca aaaatgtatt tgctataaaa 2520
tgagaagtct cactgataga ggttctttat tgctcatttt ttaaaaaatg gactcttgaa 2580
atctgttaaa ataaaattgt acatttggaa aaaaaaaaaa gccaaaaa 2627

```

## (2) INFORMATION ON SEQ ID NO. 111:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 976 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

ctcgagccgc gagattcccc cgaagttctc catgaagcgc ctcaccgccg gcctcatcgc 60
cgtcacgcgt gtgggtcgtgg tggccctcgt cgccggcatg gccgtcctgg tgatcaccaal20
ccggagaaaag tcgggggaagt acaagaaggt ggagatcaag gaactggggg agttgagaaa180
ggaaccgagc ttgtaggtac ccggcggggc aggggatggg gtgggggtacc ggatttcggg240
atcgctccag acccaagtga gtcacgcttc ctgattcctc ggcgcaaagg agacgtttat300
cctttcaaat tctgccttc cccctccctt ttgcgcacac accaggttta atagatcctg360
gcctcagggt ctcctttctt tctcacttct gtcttgaagg aagcatttct aaaatgtatc420
ccctttcggg ccaacaacag gaaacctgac tggggcagtg aagggaaggga tggcatagcg480
ttatgtgtaa aaaacaagta tctgtatgac aaccgggat cgtttgcaag taactgaatc540
cattgcgaca ttgtgaaggc ttaaagtgtt ttagatggga aatagcgttg ttatcgctt600
gggttttaaa tatttgatga gttccacttg tatcatggcc taccogagga gaagaggagt660
ttgttaactg ggccatgta gtagcctcat ttaccatcgt ttgtattact gaccacatat720
gcttgctact gggaaagaag cctgtttcag ctgcctgaac gcagtttgga tgcctttgag780
gacagacatt gcccggaaac tcagtctatt tattcttcag cttgccctta ctgccactga840
tattggtaat gttctttttt gtaaaatgtt tgtacatatg ttgtctttga taatgttgct900
gtaatttttt aaaataaaac acgaatttaa taaaatatgg gaaaggcaca caaaaaaaaa960
aaaaaaaaaa aaaaac

```

976

## (2) INFORMATION ON SEQ ID NO. 112:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1427 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing



(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

cttcgggggt gactgectct tccagggcgg gcgggtgtggt gcacgcattg ctgtgctcca 60
actccctcag ggccctgtgtt gcgcgactct gctgctatga gcttcctcaa aagtttccc 120
ccgcctgggc cagcgggagg gctcctgcgg cagcagccag acaactgaggc tgtgctgaac 180
gggaaggggc tcggcactgg taccctttac atcgctgaga gccgcctgtc ttggttagat 240
ggctctggat taggattctc actggaatac cccaccatta gtttacatgc attatccagg 300
gaccgaagtg actgtctagg agagcatttg tatgttatgg tgaatgccaa atttgaagaa 360
gaatcaaaaag aacctgtttg tgatgaagaa gaggaagaca gtgatgatga tgttgaacct 420
attactgaat ttagatttgt gcctagtgtat aaatcagcgt tggaggcaat gttcactgca 480
atgtgcgaat gccaggcctt gcatccagat cctgaggatg aggattcaga tgactacgat 540
ggagaagaat atgatgtgga agcacatgaa caaggacagg gggacatccc tacattttac 600
acctatgaag aaggattatc ccatctaaca gcagaaggcc aagccacact ggagagatta 660
gaaggaatgc tttctcagtc tgtgagcagc cagtataata tggctggggg caggacagaa 720
gattcaataa gagattatga agatgggatg gaggtggata ccacaccaac agttgctgga 780
cagtttgagg atgcagatgt tgatcactga aaatgattta tgcaagttta agattctgct 840
cctaagtgtg ggagagaact tggtgectct tccactctgg agtgaagtta atgaaagtct 900
ttttcctttt ccaaaaaccca acctgaacca gttctttctt gagacagact atactgagac 960
aacaagttgt caccagcaga agatagataa tatgaccttt attaaacttga tgaattaaact 1020
taaccaagag ggtatttgtg gtttactatt taccctaaaa ctttctgtgt ctgggtacccl 1080
tctgagtagg cctataattc ctaccttgac tgtgtgcatc atttgtaagc tagcagatct 1140
atgtggtgaa aatgcacagg agcttggtag actgcggggg aaagagagag ctcttttcgc 1200
catgttttac cagtctgctg ttataacctc ttaggttgta tcctttaatt tccagccttt 1260
taggttagtt tctgtaacag aacaagttag tctgggatga agtccctcaa gtacttcaaa 1320
tggttaattg tttgtttttg taatagctta acaataaac ctaggttttc tatattaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaggtacctg ccctaataat attctgc 1427

```

(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2639 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ccccatctct acccttcccg attctccttt tttcttttct ttttttatat ggctttcttc 60
ttttctttct ttcttttttc ttcccctttt tatttgacca gtgtaaaataa caaacattta 120
ttggtgtcac ttatggtaga aaaaacttcc tacaccagat gcacatgacc cagttgttaa 180
atagaacatt ttgaagggtga acacacaccc taaccaggt tttttaccog ctttttaaga 240
tggtccaatc ttcttctccc cccaccccaa agacatgtga gcaactgcta atgaaaagca 300
gtaaacagcc gcttaggcta tagcagtttc aactccactc tgagggtgaag attccaatta 360
cattcgagac ttaagttctt tcaatttttt cctaacaaaa gtccctgagt ccagtattta 420
caatattaca gcaactgcag atcagtgctt acaactcatc ttttctgct gtatcctctt 480
caccagttgg gggaggggct gcacttccat agagtttgct gataattggt tgaacaattt 540
cttccagttc cttcttctta gctttgaagt cttcaatgtc agcatcttgg tggctttcca 600
gccattcaat cttttcttct acagcttttt ccattggtct cttatcttca gaggaaagt 660
tacctccag cttttcttta tctccaatct gattctttag agaattaggca tagctttcca 720
actcatttct agtatcaatg cgctccttga gctttttgtc tccctcagca aacttctcag 780
catcattaac catcctttcg atttcttcag gtgtcaggcg attctgggtc ttggtgattg 840
tgatcttatt tttgttccct gtacccttgt cttcagctgt cactcgaaga ataccattca 900
catctatctc aaagggtgact tcaatctgtg ggacccacag aggagcagga ggaattccag 960
tcagatcaaa tgtaccaga agatgattgt cttttgtcag gggcttttca cttcataga1020
ccttgattgt aacagttgtg tgattatcag aagctgtaga aaagatctga gacttcttgg1080
taggcaccac tgtgttccct ggaatcagtt tgggtcatgac acctcccaca gtttcaatac1140
caagtgtaa gggacataca tcaagcagta ccagggtcacc tgtatcttga tcaccagaga1200
gcacaccagc ctggacagca gcaccatacg ctacagcttc atctgggttt atgccacggg1260
atggttccct gccattgaag aactctttaa cagtttgctg aatctttgga attcgagtcg1320
agccaccaac aagaacaatt tcatcaatat cagacttctt caaatcagaa tcttccaaca1380
ctttctggac gggcttcata gtagaccgga acagatccat gttgagctct tcaaatgttg1440
cccgagtcag ggtctcagaa aagtcttctc cttcatagaa ggactcaatt tcaattcttg1500
cttgatgctg agaagacagg gcccgtttgg ccttttctac ctgcgcgcgg agtttctgca1560
cagctctatt gtcttctctg acatctttgc cgtcttctt tttgtacagt ttgatgaagt1620
gttccatgac acgctgggtc aagtcttctc caccagatg agtatctcca ttagtggcca1680
caacttcgaa gacaccattg tcaatgggtg gaagagacac atcgaagggt ccgccaccca1740
ggtcaaacac caggatgttc ttctccccct cctcttctatc caggccataa gcaatagcag1800
ctgccgtagg ctggttgatg atcctcataa catttaggcc agcaatagtt ccagcgtctt1860
tggttgcttg gcgttgggca tcattaaaaat aggttggtac agtaacaact gcattgggta1920
ccttctttcc caaataagcc tcagcgggtt ctttcatttt agtgagaacc atggcagaaa1980
tttcttcagg agcaaatgtc tttgtttgcc cacctccaat atcaacttga atgtatggtt2040
tagttttctt ttcaaccacc ttgaacggca agaacttgat gtctgtctgc acagacgggt2100
cattccacgt gcggccgatg agccgcttgg cgtcaaagac cgtgttctcg gggttggagg2160
tgagctgggt cttggcggca tcgccaatca gacgttcccc ttcaggagtg aaggcgacat2220
aggacggcgt gatgcgggtg cctgagctgt tggcagatg ctccacgcgg cgttcttga2280
acacgcgcgc gcaggagtag gtggtcccca ggtcgatgcc gaccaccgtg cccacgtcct2340
ccttcttgte ctctctctcg gccgcgcgcg cgctgagcag cagcagcatc gcggccacca2400
gggagagctt catcttgcca gccagttggg cagcagcagg cagtccagcc acaggccgta2460
gcacaggagc acagcgcaat ttccgacttg caggcggcag gggcccgggg tcacaaggcg2520
ccacgaacca ggcgaaaggc aggtctagaa atacaggccg cggcgttcc ctctcacact2580
cgcgaaacac cccaataggt caatctgtct gtgtctgtct ggccggcctc gaccttag 2639

```

## (2) INFORMATION ON SEQ ID NO. 114:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 634 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ctccccgcgcg cgcggttaaa tccccgcacc tgagcatcgg ctcacacctg caccocgccc 60
gggcatagca ccattgcctgc ttgtcgcccta ggcccgctag ccgcgcgcct cctcctcagc120
ctgctgctgt tcggcttcac cctagtctca ggacacaggag cagagaagac tggcgtgtgc180
cccgagctcc aggttgacca gaactgcacg caagagtgcg tctcggacag cgaatgcgcc240
gacaaacctca agtgcctgcag cgcgggctgt gccaccttct gctctctgcc caatgataag300
gagggttctt gccccaggt gaacattaac ttccccagc tcggcctctg tcgggaccag360
tgccaggtgg acagccagtg tcctggccag atgaaatgct gccgcaatgg ctgtgggaag420
gtgtcctgtg tcaactcccaa tttctgagct ccagccacca ccaggctgag cagtggaggag480
agaaagtctt tgccctggccc tgcctctggt tcagccccc ctgccctccc ctttttcggg540
actctgtatt cctctctggg ctgaccacag cttctccctt tcccaaccaa taaagtaacc600
actttcagca aaaaaaaaaa aaaaaaaaca aaaa 634
```

## (2) INFORMATION ON SEQ ID NO. 115:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 719 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

gtcgactttt tttttttttt ttttaacatgg aaaagtattt ttaaaaaatcg aataatccta 60
ttcaagtcaa ccagtggttaa ccccggtgtg ctccctgcca gtctgttctt ccccatggga120
gtcacacaaa atgaaaaatct cctagaaaaga gaagacaaaag acccgcaaaa gatgtatgcc180
accatctatg agctgaaaaga agacaagagc tacaatgtca cctccgtctt gttaggaaa240
aagaagtgtg actactggat caggactttt gttccaggtt gccagcccg ggaagttcac300
ctgggcaaca ttaagagtta ccctggatta acgagttacc tcgtccgagt ggtgagcacc360
aactacaacc agcatgctat ggtgttcttc aagaaagtgt ctcaaaacag ggagtacttc420
aagatcacc tctacgggag aaccaaggag ctgacttcgg aactaaagga gaacttcac480
cgcttctcca aatctctggg cctccctgaa aaccacatcg tcttccctgt cccaatcgac540
cagtgtatcg acggctgagt gcacaggtgc cgcagctgc cgcaccagcc cgaacaccat600
tgagggagct gggagaccct cccacagtg ccacccatgc agctgtctcc caggccaccc660
cgctgatgga gccccacctt gtctgctaaa taaacatgtg cctcaaaaaa aaaaaaaaaa 719

```

## (2) INFORMATION ON SEQ ID NO. 116:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 494 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:**

```

gtcgataacg ccagacgcaa gacgcggggc ctacagcggg agcgtgagga aagccgtgcg 60
ttgcgttcca aggcattctgt gagcccgagg agtatacacc atgagcaaaag ctcaccctcc120
cgagttgaaa aaattttatgg acaagaagtt atcattgaaa ttaaattggtg gcagacatgt180
ccaaggaata ttgcgggggat ttgatccctt tatgaacctt gtgatagatg aatgtgtgga240
gatggcgact agtggacaac agaacaatat tggaatgggtg gtaatacagag gaaatagtat300
catcatgtta gaagccttgg aacgagtata aataatggct gttcagcaga gaaacccatg360
tcctctctcc atagggcctg ttttactatg atgtaaaaat taggtcatgt acattttcat420
attagacttt ttgttaaata aacttttgta atagtcaaaa aaaagtttg tctcatctac480
cttataatat ctgc

```

494

**(2) INFORMATION ON SEQ ID NO. 117:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1065 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing

**(iii) HYPOTHETICAL:** NO

**(iii) ANTI-SENSE:** NO

**(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

**(vii) OTHER ORIGIN:**

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:**

```

acgcgggtga ctacgctcaa agctccattg ttagatcctt tctgtcctcc ttcttggtctc 60
ctccttccctc cccacccctc taataggctc ataagtgggc tcaggcctct ctgcgggggtc 120
cactctgcgc ttcaccatgg ctttcattgc caagtccctc tatgacctca gtgccatcag 180
cctggatggg gagaaggtag atttcaatac gttccggggc agggccgtgc tgattgagaa 240
tgtggcttcg ctctgaggca caaccacccg ggacttcacc cagctcaacg agctgcaatg 300
ccgctttccc aggcgcctgg tggctcttgg cttcccttgc aaccaatttg gacatcagga 360
gaactgtcag aatgaggaga tcctgaacag tctcaagtat gtccgtcctg ggggtggata 420
ccagccacac ttcacccttg tccaaaaatg tgaggtgaat gggcagaacg agcatcctgt 480
cttcgcctac ctgaaggaca agctccctca ccttatgat gacccatttt cctcatgac 540
cgatcccaag ctcatcattt ggagccctgt gcgcgcgtca gatgtggcct ggaactttga 600
gaagtccctc atagggcgcg agggagagcc cttccgacgc tacagccgca ccttcccaac 660
catcaacatt gagcctgaca tcaagcgctt ccttaaagtt gccatataga tgtgaactgc 720
tcaacacaca gatctcctac tccatccagt cctgaggagc cttaggatgc agcatgcctt 780
caggagacac tgctggacct cagcattccc ttgatatoag tccccttcac tgcagagcct 840
tgcccttccc ctctgcctgt ttccttttcc tctcccaacc ctctgggttg tgattcaact 900
tgggctccaa gacttgggta agctctgggc cttcacagaa tgatggcacc ttcctaaacc 960
ctcatgggtg gtgtctgaga ggcgtgaagg gcctggagcc actctgctag aagagaccaa1020
taaaagggcag gtgtggaata aaaaaaaaaa aaaaaaaaaa aaaaaa

```

1065

**(2) INFORMATION ON SEQ ID NO. 120:**

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 648 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:
- (vii) OTHER ORIGIN:  
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggactgccgt cgtagtctc cggcgagttg ttgcctgggc tggacgtggt tttgtctgct 60
gcgcccgcctc ttgcgcctct cgtttcattt tctgcagcgc gccagcagga tggcccacaa120
gcagatctac tactcggaca agtacttcga cgaacactac gagtaccggc atgttatgtt180
acccagagaa ctttccaaac aagtacctaa aactcatctg atgtctgaag aggagtggag240
gagacttggg gtccaacaga gtctaggctg gggttcattac atgattcatg agccagaacc300
acatattctt ctcttttagac gacctcttcc aaaagatcaa caaaaatgaa gtttatctgg360
ggatcgtcaa atctttttca aatttaaatgt atatgtgtat ataaggtagt attcagtga420
tacttgagaa atgtacaaat ctttcatcca tacctgtgca tgagctgtat tcttcacagc480
aacagagctc agttaaatgc aactgcaagt aggttactgt aagatgttta agataaaaagt540
tcttcagtc agtttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaag tttgtatgtt gcatttaaaa aaaaaaaaaa aaagtcga 648

```

(2) INFORMATION ON SEQ ID NO. 121:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 1842 base pairs  
 (B) TYPE: Nucleic acid  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual  
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:  
 (A) ORGANISM: HUMAN  
 (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```

ctcgagccgc tcgagccgct gctctctgga gggggtagag atcaaaggcg gtccttccg 60
acttctccaa gagggccagg cactggagta cgtgtgtcct tctggcttct acccgtaacc 120
tgtgcagaca cgtacctgca gatctacggg gtccctggagc accctgaaga ctcaagacca 180
aaagactgtc aggaaggcag agtgcagagc aatccactgt ccaagaccac acgacttcga 240
gaacggggaa tactggcccc ggtctcccta ctacaatgtg agtgatgaga tctctttcca 300
ctgctatgac ggttacactc tccggggctc tgccaatcgc acctgccaag tgaatggccg 360
gtggagtggg cagacagcga tctgtgacaa cggagcgggg tactgtcca acccgggcat 420
ccccattggc acaaggaagg tgggcagcca gtaccgcctt gaagacagcg tcacctacca 480
ctgcagccgg gggcttacct tgcgtggctc ccagcggcga acgtgtcagg aaggtggctc 540
ttggagcggg acggagcctt cctgccaaaga ctcttcatg tacgacaccc ctcaagaggt 600

ggccgaagct ttctgtctt cctgacaga gaccatagaa ggagtcgatg ctgaggatgg 660
gcacggccca ggggaacaac agaagcggaa gatcgctcctg gacccttcag gctccatgaa 720
catctacctg gtgctagatg gatcagacag cattggggcc agcaacttca caggagccaa 780
aaagtgtcta gtcaacttaa ttgagaaggt ggcaagttat ggtgtgaagc caagatatgg 840
tctagtgaca tatgccacat accccaaaat ttgggtcaaa gtgtctgaag cagacagcag 900
taatgcagac tgggtcacga agcagctcaa tgaaatcaat tatgaagacc acaagttgaa 960
gtcagggact aacaccaaga aggccctcca ggcagtgtac agcatgatga gctggccaga 1020
tgacgtccct cctgaaggct ggaacgcac ccgccatgtc atcatcctca tgactgatgg 1080
attgcacaac atggggcggg acccaattac tgtcattgat gagatccggg acctgctata 1140
cattggcaag gatcgcaaaa acccaaggga ggattatctg gatgtctatg tgtttggggt 1200
cgggcctttg gtgaaccaag tgaacatcaa tgctttggct tccaagaaag acaatgagca 1260
acatgtgttc aaagtcaagg atatggaaaa cctggaagat gttttctacc aaatgatcga 1320
tgaaagccag tctctgagtc tctgtggcat ggtttgggaa cacaggaagg gtaccgatta 1380
ccacaagcaa ccatggcagg ccaagatctc agtcattcgc ctttcaaagg gacacgagag 1440
ctgtatgggg gctgtggtgt ctgagtactt tgtgctgaca gcagcacatt gtttactgt 1500
ggatgacaag gaacactcaa tcaaggtcag cgtaggaggg gagaagcggg acctggagat 1560
agaagtagtc ctatttcacc ccaactacaa cattaatggg aaaaaagaag caggaattcc 1620
tgaattttat gactatgacg ttgccctgat caagctcaag aataagctga aatatggcca 1680
gactatcagg cccatttgtc tcccctgcac cgagggaaca actcgagctt tgaggcttcc 1740
tccaactacc acttgccagc aacaaaagga agagctgctc cccgcagaag agcaaaagaa 1800
gotgtgtttg tccgggggga gaaaaaaacc gccccggggg gg
1842

```

## (2) INFORMATION ON SEQ ID NO. 122:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```

ggcgggtata aaagccccac ccaggccagc cggctctgct cagcatttgg ggacgtcttc 60
agctctcggc gcacggccca gcttccttca aaatgtctac tgttcacgaa atcctgtgca 120
agctcagctt ggagggtgat cactctacac cccaagtgc atatgggtct gtcaaagcct 180
atactaactt tgatgctgag cgggatgctt tgaacattga aacagccatc aagaccaaag 240
gtgtggatga ggtcaccatt gtcaacattt tgaccaaccg cagcaatgca cagagacagg 300
atattgcctt cgccctaccag agaaggacca aaaaggaact tgcatacagca ctgaagtcag 360
ccttatctgg ccacctggag acggtgattt tgggcctatt gaagacacct gctcagtatg 420
acgctcttga gctaaaagct tccatgaagg ggctgggaac cgacgaggac tctctcattg 480
agatcatctg ctccagaacc aaccaggagc tgcaggaaat taacagagtc tacaaggaaa 540

tgtacaagac tgatctggag aaggacatta tttcggacac atctggtgac ttccgcaagc 600
tgatgggttc cctggcaaaag ggtagaagag cagaggatgg ctctgtcatt gattatgaac 660
tgattgacca agatgctcgg gatctctatg acgctggagt gaagaggaaa ggaactgatg 720
ttcccaagtg gatcagcatc atgacggagc ggaggggccc cactccaga aagtatttga 780
taggtacaag agttacagcc cttatgacat gttggaaaagc atcaggaaaag aggttaaagg 840
agacctggaa aatgctttcc tgaacctggt tcagtgcatt cagaacaagc cctgtattt 900
tgctgatcgg ctgtatgact ccatgaaggg caaggggagc cgagataagg tctgatcag 960
aatcatggtc tcccgccagt aagtggacat gttgaaaatt aggtctgaat tcaagagaaa 1020
gtacggcaag tccctgtact attatatcca gcaagacact aaggcgagct accagaaagc 1080
gctgctgtac ctgtgtggtg gagatgactg aagcccagca cggcctgagc gtccagaaat 1140
ggtgctcacc atgcttccag ctaacaggtc tagaaaacca gcttgccaat aacagtcctcc 1200
gtggccatcc ctgtgagggt gacgttagca ttacccocaa cctcatttta gttgcctaag 1260
cattgcctgg ccttctctgt tagtctctcc tgtaaagcaa agaaatgaac attccaagg 1320
gttggaagtg aagtctatga tgtgaaacac ttgacctcct gtgtactgtg tcataaacag 1380
atgaataaac tgaatttgta ctttagaaac acgtactttg tggccctgct ttcaactgaa 1440
ttgtttgaaa attaaacgtg cttgggggtc agctgggtgag gctgtccctg taggaagaaa 1500
gctctgggac tgagctgtac agtatggttg cccctatcca agtgtogcta ttaagttaa 1560
atttaaatga aataaaataa aataaaatca aaaaaa

```



## (2) INFORMATION ON SEQ ID NO. 123:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

gtcgcagctg accctcgcgc ccgccccgcg ctggagtcgc acgtggaagt tgctggctga 60
ctgggcttgc gaggaaccgc cctcgagctc gcagccgaag gcaaggaaac actgaagatc 120
ggcgagggag gacagggggg tcatcatggg tggctttttc tcaagtatat tttccagtct 180
gtttggaact cgggaaatga gaattttaat tttgggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaagt tgttactact atacctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaacettta attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaacaca gatgcagtca tttatgtagt 420
agacagttgt gaccgagacc gaattggcat ttccaaatca gatttagttg ccatgttgga 480
ggaagaagag ctgagaaaaa ccatttttagt ggtgtttgca aataaacagg acatggaaca 540
ggccatgact toctcagaga tggcaaattc acttgggtta cctgccttga aggacogaaa 600
atggcagata ttcaaaacgt cagcaaccaa aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagtcca ttcttctccc ctgaaatgaa 720
gactacatca cctctctccc tttggaaaca gtcaagtgtg cttcacacta ctgatgtta 780

aaactatatg attattggca tatactgact gactgcaata tttgtagtaa atagggaaaa 840
taagtattta gttggagggg taatttgatc gaatcacctg aatgttctat gtaatgtaaa 900
atatcttttt cttgctttct tgtgttaagg tatatatctt atttgtatgg aattcttatt 960
caaatacagt tctattaaag agtatactcc tattggatga aaaaaaccta aaaaaaaaaa 1020
aaaaaaaaaa aaa                                     1033

```

## (2) INFORMATION ON SEQ ID NO. 124:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ICLLVHFEVSR AKTVNLTFY WWVITENKDL FSCSLKSHK NNQIGSCLLS CVSWFLTCVH60  
TPVCL 65

(2) INFORMATION ON SEQ ID NO. 125:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ISVFRLEFKYL THFQTCTMFY KPLDFQQHTI ENTCYSKHNF SVSSIAVVRD NIAISGMLQA60  
FKIA 64

(2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

KANLLPATPE GTQIWVGPFV QLGKRMGKPG DGFHKFSSGL WHSFQEIPLG KGLLANMHFQ60  
T 61

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

LKNTNEVKAL NWYTLFTPIF QVWKCIFASR PLPRGISWKE CHNPLENLWK PSPGFPIRLP60  
 SWKTGPTHIW VPSGVAGRRF AF 82

## (2) INFORMATION ON SEQ ID NO. 128:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

HTWDPYPLGI SPRTIRPVCQ PKVAFGMLNF PLSKKVHLPN EVTIRLNPCK SLDFVFYKNS60  
 TFPKSLVIK ISTLPKCDST AWFLANKNPI 90

## (2) INFORMATION ON SEQ ID NO. 129:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

MVADYGCTIL ILGPFTHRNH TKWPDITYFTE QFKYYTLAKS TYSTHPGEGG EKTHTYKTTS60  
LDTMCLPTIS SLNNFHQLRC LV 82

(2) INFORMATION ON SEQ ID NO. 130:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 70 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

RNLVTQMKSG IEDPWTQVQN ADYSLAFPLY LCKEGYTELI LFQAYNFKFY HLNSSTFAAE60  
EWNQKNVVSF 70

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 60 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

AIQCEAYFIA TLVDCQGDSA TVLDKLMFPF SLAANRRATY SAGSRARSWG SRGYTSSLII60

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 181 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLLQAAPGAP RPSSSTLVDE LESSFEACFA 60  
 SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFLLQ KRLQLSVQKP EQVIKEDVSE120  
 LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180  
 T 181

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 423 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

LSEDEIRTLK QKKIDETSEQ EQKHKETNNS NAQNPSEEEG EGQDEDILPL TLEEKENKEY 60  
 LKSLFEILIL MGKQNIPLDG HEADEIPEGL FTPDNFQALL ECRINSGEEV LRKRFETTAV120  
 NTLFCSKTQQ ROMLEICESC IREETLREVR DSHFFSIITD DVVDIAGEEH LPVLVRFVDE180  
 SHNLREEFIG FLPYEADAEI LAVKFHTMIT EKWGLNMEYC RGQAYIVSSG FSSKMKVVAS240  
 RLLEKYPQAI YTLCCSCALN MWLAKSVPM GVSVALGTIE EVCSFFHRSP QLLLELDNVI300  
 AVLFQNSKER GKELKEICHS QWTGRHDAFE ILVELLQALV LCLDGINSMT NIRWNNYIAG360  
 RAFVLCSAVS DFDFTVITIV LKNVLSFTRA FGKNLQGQTS DVFFAAGSLT AVLHSLNEVS420  
 GKY 423

## (2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 237 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

VENIEVYHEF WFEEATNLAT KLDIQMKLPG KFERRAHQGNL ESQLTSESYY KETLSVPTVE 60  
 HIIQELKDIF SEQHLKALKC LSLVPSVMGQ LKFNTSEHH ADMYRSDLPN PDTLSAELHC120  
 WRIKWKHRGK DIELPSTIYE ALHLPDIKFF PNVYALLKVL CILPVMKVEN ERYENGRKRL180  
 KAYLRNTLTD QRSSNLALLN INFEDIKHDLD LMVDITYIKLY TSKSELPTDN SETVENT 237

## (2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

- RIRINGSLCP QTKNNLYFHI VELSIGASV GERWYGMGES ILPARGESQG LLCLYFYKEI60  
 LPLFLVNKLR GTDVGLEQGL SGGEGSWTA 89

## (2) INFORMATION ON SEQ ID NO. 136:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

EEERAKREEL ERILEENNRK IAEAQAKLAE EQLRIVEEQR KIHEERMKLE QERQROQKEE60  
QKIILGKGKS RPKLSFSLKT QD 82

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 71 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

SALKVEYLLS CPVSCRVCSS AAIRASFLFK MICTVSLAIP ASAAQPFIKK QHTRKAELRN60  
ADVYGKKEQK M 71

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

SSAQRKYFNL PVEILVMERC QTVLNGRTSK SEATVPPTTRG LLYCSTFSAL YFLAEASPWS60  
AMYKLGY 67

## (2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 49 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

RAEKVEQYKS PRVVGTVASL LLVLPFKTVW HLSMTRISTG RLKYFLCAE

49

## (2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

SCERRGFIMA DDLKRFLYKK LPSVEGLHAI VVSDRDGVPV IKVANDNAPE HALRPGFLST 60  
 FALATDQGSK LGLSKNKSII CYYNTYQVVQ FNRLPLVVSF IASSSANTGL IVSLEKELAPI20

LFEEELRQVVE VS

132

## (2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

QMIILFLESP SLLPWSVARA KVDKKPGRKA CSGALSFATL ITGTPSLSDT TMAWSPSTLG 60  
NFLYKNRFRS SAMMNPLLSQ DQSPRLGFLG CLVLSAVTSG TALKTGSSSS HRHMIHDLVC120  
APGSTF 126

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 152 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

SAVKRGWDLN MAAVVAATAL KGRGARNARV LRGILAGATA NKASHNRTRA LQSHSSPECK 60  
EEPEPLSPEL EYIPRKRKGN PMKAVGLAWA IGFPKGILLF ILTKREVDKD RVKQMKARQN120  
MRLSNTGEYE SQRFRASSQS APSPDVGSQV QT 152

(2) INFORMATION ON SEQ ID NO. 143:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 114 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

EGRSAPQVCT PDPTSGDGAL WEEALNLWLS YSPVLDNRMF CRAFTCFTRS LSTSRIVRMK 60  
RRIPQGKPMQ QASPTAFMGF LPLFLGMYSS SGDRSGGSSL PSGELWLCRA RVLL 114

## (2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 267 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

EDEVEEEESTA LQKTDKKEIL KKSEKDTNSK VKPKGKVRWT GSRTGRWKY SSNDESESG 60
SEKSSAASEE EEEKESEEAI LADDDPECKK CGLPNHPELI LLCDS CSGY HTACLRPPLM120
IIPDGEWFCP PCQHKLLCEK LEEQLQDL DV ALKKKERAER RKERLVYVGI SIENIIPPQE180
PDSFSEDQEEK KKDSKSKAN LLERRSTRTR KCISYRDEF DEAIIDEAIED DIKEADGGGV240
GRGKDSTIT GHRGKDISTI LDEKIIT                                     267

```

## (2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 185 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RRQAVWYPLS QESHRRISG WFGPHFLHG SSSSARMASS LSFSSSSSEA120
ADDFSLPDPS LSSLLEYFHL PRVREPVRT LPLGFTLEFV SFSDFFKISF LSVFCKAVDS180
SSTSS                                             185

```

## (2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 134 amino acids
  - (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

KRQPTSAMKD PSRSSTSPSI INEDVIINGH SHEDDNPEAE YMWMEEEEF NRQIEEELWE 60
EEFIERCFQE MLEEEEEHEW FIPARDLPQT MDQIQDQFND LVISDGSSLE DLVVKSNLNP120
NAKEFVPGVK YGNI                                     134

```

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 135 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

HSDKRAFTIK SSNTAFTVWK LCYIHQKRAP STQIFPYFTP GTNSFAFGFR LLLTTRSSRE 60
EPSLITRSLN WSWIWSIVCG RSRAGINHSC SSSSSSISWK QRSINSSSHN SSSICLLNSS120
SFSIHMYSAN GLSSS                                     135

```

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 58 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

LVSGANQCGS CNSKSFLTKA WYYRVGFRFF RGGLFDFDFE FFYVIFGKTH SELYLVT 58

## (2) INFORMATION ON SEQ ID NO. 151:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

FFVLKSLLVG ACYWEQVFVQ KLQSESLCIT ETLFITSLLS LPQKTVGLNK IICILIYLC60  
L 61

## (2) INFORMATION ON SEQ ID NO. 152:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 60 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

SACKFLRDLF LLTVDQLMYT CIIKALNKSL WLITAKMGTR HLLCVLVTAV ALRAVRPCL160

## (2) INFORMATION ON SEQ ID NO. 153:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids

(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

KRDIILNVFS QRSHKRKKNQ NQINHHEKNE TPHGNTKLWL GSSYYYSSHI GWRKRP 56

(2) INFORMATION ON SEQ ID NO. 155:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 150 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

IPVHRLHGRA DPLGWSIVSD LITSGLGAGV LRGLPARRLH SLGRRVLGRP GVLRLGLHG 60  
 RRDALGAWSA AQRPRTPGRP ACVCAPRRGP ESPSADPVPP PGRAGDPSPD DASASGPRGG120  
 AATKAGPAHD PGQLRPELRV LPPPPRGDRE 150

(2) INFORMATION ON SEQ ID NO. 156:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 81 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

LPVAAGGRGQ DAQLRPESLG VVSRPRLGGG APSRSRGRRI GVARVSSPAG RRDRVCGGGL60  
 GASAGRAHAG GAARGAGPLR G 81

## (2) INFORMATION ON SEQ ID NO. 157:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 214 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

PGSQSVTPPM AEPLQPDPGA AEDAAAQAVE TPGWKAPEDA GPQPGSYEIR HYGPAKWVST 60  
 SVESMDWDSA IQTGFTKLNS YIQGKNEKEM KIKMTAPVTS YVEPGSGPFS ESTITISLYI120  
 PSEQQFDPPR PLESDVFIED RAEMTVFVRS FDGFSSAQKN QEQLLTLASI LREDGKVFDE180  
 KVVYTAGYNS PVKLLNRNNE VWLIQKNEPT KENE 214

## (2) INFORMATION ON SEQ ID NO. 158:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

PNFYRGFIFN LTMCGGLSCL NLFRAVCSVH QMGRSGMGHL RPFRSGLNRM LEPRLDSDTL60  
 RF 62

## (2) INFORMATION ON SEQ ID NO. 159:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 104 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

IHLPPKKLISF YLRGEVQFSF GSSESKHLIC WVKWTPFLAF YVLSHNNSIK QEGKQKTKKK 60  
KGKKKNLHGL VSLTKHVGAV CLGGAGYRTC QCLGFSINLA RDIK 104

(2) INFORMATION ON SEQ ID NO. 160:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

SLGISRKIKQ NTSPARLTCV YIYIKQRATP TSQQLGEISA VHAVVCQFGE ITPWKNWKNL60  
LAGKNSFICI KSVLQKNPCG 80

(2) INFORMATION ON SEQ ID NO. 163:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

PSIDLEAEES QRLLKVVMWF SFKKLLFLES RIYGYNVCSL FVHKIKPFKK LKKKKKRGEK60  
 KREKGGKGRK RRGE 75

## (2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 68 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

KYLTLPYKLL VPFCIPPSIT LTKGIFYCKE YFILIYTSHE FLPLVTIQML PSIIQIAQP60  
 FYVHNSLL 68

## (2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

LFFLFRYHTV PLPPKGRVLI HWMTLCQTQM KLMAIPLVFQ IMFGILNGLY HYAVFEETLE60  
 KTIHEE 66

## (2) INFORMATION ON SEQ ID NO. 166:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 159 amino acids



(B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TRLKGDRGGV HFLKALRRGG LRASLLYLLE KYRLVFLLSI CVRGMVSSVK SFLVGEQLLS 60  
 ISEPRFKMSV CKCSFLSTTS TFPVPISSDSK KVSSYFSLCS ESLAEQNLFM MPEVFCSEQK120  
 FDPENLDSF FFTRLFSSLV TLRVSPHAPA SEMQTVLSS 159

(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 439 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

KSLLETSSKF PLISFSSPQG LKFRSKSSLA NYLHKNGETS LKPEDFDFTV LSKRGIKSRV 60  
 KDSCMAALTS HLQNSNNNSN WNLRTSRKCK KDVFMPSSSS SELQESRGLS NFTSTHLLK120  
 EDEGVDDVNF RKVRKPKGKV TILKGPIKK TKKGCRKSCS GFVQSDSKRE SVCNKADAES180

EPVAQKSQLD RTVCISDAGA CGETLSVTSE ENSLVKKKER SLSSGSNFCS EQKTSGLINK240  
 FCSAKDSEHN EKYEDTFLES EEIGTKVEVV ERKEHLHTDI LKRGSEMDNN CSPTRKDFTE300  
 OTIPRTOIER RKTSLYFSSK YNKEALSPPR RKAFKKWTPP RSPFNLVQET LFHDPWKLLI360  
 ATIFLNRTSG KMAIPVLWKF LEKYPSAEVA RTADWRDVSE LLKPLGLYDL RAKTIVKFS420  
 EYLTQWKYP IELHGIGAP 439

## (2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 90 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

DCGKVQTQMQ FALTNFLGLI SLCKTPVLSF LPQDRVQSFL KHALRCPHLR HCFVDTLKGV60  
 HKAKKSDQML RASNLYLTTW TWHWQKSLQH 90

## (2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

SDFCQCHVQV VRYKLLALSI WSDFFALWTP LRVSTKQCLR CGHLRACFRK LCTLSCGRKE60  
 RTGVLHKEIS PRKLVNANCI CVCTL PQSYI VF 92

## (2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 91 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

ADSHQNYIPW PPACVLLARP WLASLTREKD LQKIRLWDHF VCALGMTFFP TPGKPLGLSE60  
TLWLANHMVS LKVERLSNPP IPREFQSV DV I 91

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 95 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

NGGLNAHLAS ASEFDHSGVQ LIEREEEICI FYEKINIQEK MKLNGEIEIH LLEEKIQFLK60  
MKIAEKQRQI CVTQKLLPAK RSLDADLAVL QIQFS 95

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 90 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

KTEFGAQLGR HPGTSWLAVI SGSHKEVFAS QQSSFSGIGS FLPVDVFQFL HLVSSSLGYL60  
FFHKKCIFLL PALSAERHYG QIQRQLSGH 90

(2) INFORMATION ON SEQ ID NO. 173:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

AVRSRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60  
 SPFHDIPIYA DKVRHPCFWT QSLYSDQLVL HMNFLICLST SA 102

## (2) INFORMATION ON SEQ ID NO. 174:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 73 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

VKRLCPKTRM PYLICINWNI MKWRYILSFL IFEEDSVLQG EGRGALLGAE AAHSAGVLFP60  
 PLPQSHQPAR GAD 73

## (2) INFORMATION ON SEQ ID NO. 175:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

RRQRKAEPGA CALGRVGSEC IPEPGARRTA QAAGLRVSG AANTKVRELK HFRFLGLLRS 60  
 CRSEMEVDAP GVDGRDGLRE RRGFSEGGGRQ NFDVRPQSGA NGLPKHSYWL DLWLFILFDV120  
 VVFLFVYFLP 130

## (2) INFORMATION ON SEQ ID NO. 176:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 62 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ILKMATNFLN KEDRTLNRRI SHLQGTLPFI LHFVTNLQNS INWVGHPFL AKFLKLNPLV60  
 RV 62

## (2) INFORMATION ON SEQ ID NO. 177:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 174 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

AVYCILHQQK VLRLYKRALR HLESWCVQRD KYRYFACLMR ARFEEHKNEK DMAKATQLLK 60  
 EAEZEEFWYRQ HPQPYIFPDS PGGTSYERYD CYKVPEWCLO DWHPSEKAMY PDYFAKREQW120  
 KKLARRESWER EVKQLQEETP PGGPLTEALP PARKEGDLPP LWWYIVTRPR ERPM 174

## (2) INFORMATION ON SEQ ID NO. 178:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCAV 60  
DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120  
TPFADVVCNI R 131

## (2) INFORMATION ON SEQ ID NO. 179:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60  
PPKWRQIHDL KDTQYLLNSS 80

## (2) INFORMATION ON SEQ ID NO. 180:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 140 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

KVLRKFKGPE EASQMAGAG PTMLLREENG CCSRRQSSSS AGDSGGERED SAAERARQQL 60  
 EALLNKTMRI RMTDGRITLVG CFLCTDRDCN VILGSAQEFL KPSDFSFSAGE PRVLGLAMVVP120  
 GHHIVSIEVQ RESLTGPPYL 140

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 114 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

SLKGKRHRGQ RYGGPVRLSL CTSMETMWCP GTMARPSTRG SPAEKESDGL RNSCAEPRMT 60  
 LQSRVQRKQ PTSVRPSVMR MRIVLLSSAS SCCRARSAAE SSRSPSPSPA LELL 114

(2) INFORMATION ON SEQ ID NO. 182:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RLSRLTEPKK DPMAGISTAE HHLOPTAALP TQLSRSRHSP QVISTDGGET RGCGRQERKA60  
 ERRVCKNAKV TFPIVGGKQ RHWFOCHRQS EHLEL 95

(2) INFORMATION ON SEQ ID NO. 183:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 131 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

RRVQHPPFFS QLIRDAAKRT FRITRLQAFS KYLVVYVYLN GSMLPVPSPC PLCQPPVALV 60  
 LVSFPSSAKR PWNLNGGCFA LGGSCWWDQS FDKPPAPWWH LSWKDVTPG AQTACGSRTS120  
 AFGIFLPQWG R 131

## (2) INFORMATION ON SEQ ID NO. 184:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 128 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

TAPCCRCPPAP VPSVNPLSLW CWFRSRLQQN DLGTSMGAAL LWEVLVGGTR ALTNLLLLGG 60  
 TSPGRTSQLQ VLRLPVAAEP VPLAFSSHNG EGDFGILTNS SLGLSLLPST ASRFSSICAY120  
 YLRTVSAP 128

## (2) INFORMATION ON SEQ ID NO. 185:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes



(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

DSRVYCFSGN YRKLVLPRKT GAIRNGSNIS KLRKQDVLSF AHLGFLFPF SLFSLRSLFQ60  
FPSDLPLVPL ESQRL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

LGDSESMPLL ALKCPVRLLG TLEPSEILII LGSSPYFQMF SAQHWVLSST TENPEEKGR60  
FP 62

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 89 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

PHPSRRLTQG RWVRKSRVAM EKIPVSAFLR LVALSYNLAR DSTVKPGAKK DRKESRAKLR60  
QTLRSWGEQ LIWTQTYEEA LYKSRLATN 89

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 72 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GNPELPWRKF QCQHSCALWR SPTIWPGIAQ SNLEPKRTGR SLEPNCARPS PEVGVNNSG60  
LRRMKKLYIN RD 72

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 125 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

SLGHRPRNGG HSRGCDLGGL HAHSPDPRLO GAGLQOAKNA AYSVSLPPGC VGHLWPHLRL 60  
HHRTGREHRA HTLLPLWDPL FHLLLLPAGS CCQSDQARPG EEAPFPVGDS GSGRGLQSP120  
GCYRY 125

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 200 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

RGRDSCPRSP PALRSSPAAL LRAGSSTKFT ANALALGSRM ATTVPDGCNR GLKSKYYRLC 60  
 DKAEAWGIVL ETVATAGVVT SVAFMLTLPI LVCKVQDSNR RKMLPTQFLF LLGVLGIFGL120  
 TFAFIIGLDG STGPTRFFLF GILFSICFSC LLAHAVSLTK LVRGRKPLSR LVILGLAVGF180  
 SLVQDVIAIE YIVLTMNRTK 200

## (2) INFORMATION ON SEQ ID NO. 191:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

AEAHGQTQNH QPGKGLPPPD ELGQTDMSQ QAGEADGKED PKEEEACGPC APVQSDDEGE 60  
 GEAKDAQHTQ EEEKLSRQHF SPVGVHLHAD EDRESEHEGH RGHNP GCGHR F 111

## (2) INFORMATION ON SEQ ID NO. 192:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

EIYWETDYNH SGTIDAHMR TALRKAGFTL NSQVQQTIAL RYACSKLGIN FDSFVACMIR60  
 LETLFKLFSL LDEDKDG MVQ LSLAEWLCCV LV 92

## (2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 81 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ESLIAFLFLH DQCAQDSIVL TMIKDVVRIQ WTRNECKGGL EQRRGCPEGK ESYQILLNLQ60  
 PERLEFHRPQ SAPFHCSRHI K 81

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

KTTHGPGQN HLPFPHCFLK RPTLSKGGP IDSSQEGFRA SIRAWPVLAP LLSEQQGFGG60  
 SGWHESLSLP SCSFMTNVPR TQ 82

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

RPPPSRSSL AGQTNTQHS SARES

25

## (2) INFORMATION ON SEQ ID NO. 196:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 71 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TMPSSLSSRR LNSLKRVSR IIQATKLSKL MPSLLHAYRR AMVCCTWLLR VKPAFLRAVL60  
ISWASMVPEW L 71

## (2) INFORMATION ON SEQ ID NO. 197:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

IRRNTSRISV HTWRRTPPYD SPACFSCSIV SLEGSGFFSC VSVFFSFDLS NFSISAISGL60  
SDMVAEEKQS EAHEYERQFL ASRRSG 86

## (2) INFORMATION ON SEQ ID NO. 198:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 101 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

HPFSTFPTLP PQAGKFDATL LASQCILGGA RLLTIRLLAS PVQSFLWKAV DFSLASLSSS 60  
 VSTYRISR SQ PYRVCQTWLR RKSKARTST SDSSSR LAAV A 101

## (2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TPFPSPQLYP LKQVNSTQHF SHLSAYLA AH ASLRFACLLL LFNRFEGROW IFLLRLCLLQ 60  
 FRLIEFLDLS HIGFVRHGCG GKAKRGARVR ATVPRVSPQW 100

## (2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 153 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GLTDQYLELN ALQEEELGPFQ LVILGFPSNQ FGKQEPGENS EILPSLKYYR PGGGFVVPNFQ 60  
LFEKGDVNGE KEQKFYTFK NSCPPTAELL GSPGRLEWEP MKIHDIRWNF EKFLVGPDGI120  
PVMRWYHRTT VSNVKMDILS YMRRQAALSA RGK 153

(2) INFORMATION ON SEQ ID NO. 201:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 249 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

LMPPFPYPYPL PIMQGPRRGS SGRKPHSQSF YPHPRFSFLL HKRQAWHNCV SEPLWTRDNC 60  
PSVCMATQPR ICLLETQGS ICVYGLAQHP HIFFSFLFQM SPKETQVLGP MVLLKPEHHS120  
WGQHLPHAHT THHQPPSSFL KDPPEPPSPS HSAPETSQDN CERDGRVPQV RGGVSMKEGP180  
EALVGGPPLS PSVVPALSAF RLRLPGRDTP PAPLEDMLSS HSVHWYLNTP ICPVKVFLQQ240  
KKKKKKKKK 249

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

AGLSAPPPAP LLCRAQAPLA LGSNFSYRHS VRPGSSPGAH LPEARCGGGP RGRSQAQSPQ 60  
 SSGPVGGGRGR SGSKARTPQL FRLQQQLQRF GHGCEVPCW LQAAREHPGQ GQEAQSEEEG120  
 EGQEGEGQEE GGSPLKGPQ GSNLPLCLR VPTTWS 156

(2) INFORMATION ON SEQ ID NO. 203:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

DPTSLTAMEF DLGAALPTS QKPGVGAGHG GDPKLSPHKV QGRSEAGAGP GPKQGHSSS 60  
 DSSSSSSSDSD TDVKSHAAGS KQHSIPGKA KPKVKKKKEK GKKEKGKKKE APH 113

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 162 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

GGPPPPKHLs SRWLVLVGRE EGLMSPVQGP SVGSLLLLLAL LLLALLLLH FGLLGLARDA 60  
 LVLIGASSVG LHIRVRIAGA AAGVGRAVVS LLWTRTCPL RPALEFVGTE LGISPVARPH120  
 TGLLGGGLQG CSQVELHGGK RSWVLRPRAP GPCRGAEQGE ER 162

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 145 amino acids
  - (B) TYPE: Protein



(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
VEPWTTTCAA GAVMADYWKS QPKKFCDYCK CWIADNRPSV EFHERGKNHK ENVAKRISEI 60
KQKSLDKAKE EEKASKEFAA MEAAALKAYQ EDLKRLGLES EILEPSITPV TSTIPPTSTS120
NQQKEKKEKK KKRSFKGQMG RRHNL                                     145
```

(2) INFORMATION ON SEQ ID NO. 206:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 262 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
PALSHLPRHQ INRKKRKRRR KKDPSKGRWV EGITSEGYHY YYDLISGASQ WEKPEGFQGD 60
LKKTAVKTVW VEGLSDEGFT YYYNTETGES RWEKPDDEFIP HTSDLPSSKV NENSLGTLDE120
SKSSDSHSDS DGEQEAEEGG VSTETEKPKI KFKEKNKNSD GGSDPETQKE KSIQKQNSLG180
SNEEKSKTLK KSNPYGEWQE IKQEVESHEE VDLELPSTEN EYVSTSEADG GGEPKVVFKE240

KTVTSLGVMA DGVAPVFKKR RT                                     262
```

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 73 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

GKGRRKGIKG VCCNGGSCPE SIPRGFEKTW LRVRNFGAKH NTSNQHYPTY LDIKSTERKE60  
REEEKILQR ADG 73

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

IWNFQALKMS MYQLQKLMVA ENPKWYLKKK QSLLELWQM EWPQSSKREE LENGKILGKF60  
KGNEVMIQ 68

(2) INFORMATION ON SEQ ID NO. 210:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 194 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

SVHCFREDKM KFTIVFAGLL GVFLAPALAN YNINVNDNN NAGSGQOSVS VNNEHNVANV 60  
DNNNGWDSWN SIWDYGNQFA ATRLFQKKTC IVHKMNKEVM PSIQSLDALV KEKKLQKGKGP120  
GGPPPKGLMY SVNPNKVDDL SKFGKNIANM CRGIPTMAE EMQEASLFFY SGTCTTSVL180  
WIVDISFCGD TVEN 194

## (2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 82 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VHQALGRWSS WSLTLKLLFL DQCIKGLNGG HDFLVHFVHN ACLLLKESGC SKAISIIPDG60  
IPGVPSVVIV NIGHIVFVD TH 82

## (2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 119 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

ELGLNHLWLR VWLEPTAQVP DVLFPEFMER EEKAVSLLW FNVKEPQLPP LPGREAFGFL 60  
LLLLALVAGE VLQDHRALQ LVLAGLRAHA GRLRFRKALT KASARCAPEG WTSESFAF 119

## (2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 136 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

IICGCVSGLS PLHRSLMYCF QSSWRGRKRL YLCCSGLMSK SRSSLLCLAE KPLAFFFFSL 60  
RLWRVKYSRT TALRCWSWSSR ACGLMRGVCA SGRPSRRPRP AVLLKAGHRS HSPLSETMHG120  
RSHSSFSDRF RRLMT 136

(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TLETVHQGPV QWAQARHAAT DDSGQALKGR SSRGYYFSDK IQMPLLCGY RNPSTGNKAH 60  
FQNYHQRRPP ESYPOAKLRV HCGNRWLYFL HLREQIPASV K 101

(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 204 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

LRCPAFRSTA GRGLREGLPE AOTPRMSPQA REDQLQRKAV VLEYFTRHKKR KEKKKKAKGF 60  
 SARQRRELRL FDIKPEQQRY SLFLPLHELW KQYIROLCSG LKPDTPQPMI QAKLLKADLH120  
 GAIISVTKSK OPSYVGITGI LLQETKHIFK IITKEDRLKV IPKLNCVFTV ETDGFISYIY180  
 GSKFQLRSSE RSAKKFKAKG TIDL 204

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 645 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

PTRPVAAGSE QQQQSAFIQE RQPVALMRLI SFNVPHIKNS TGEPIWKVLI YDRFGQDIIS 60  
 PLLSVKELRD MGITLHLLH SDRDPIPDVP AVYFVMPTEE NIDRMCQDLR NQLYESYYLN120  
 FISAISSRL EDIANAALAA SAVTQVAKVF DQYLNFILE DDMFVLCNQN KELVSYRAIN180  
 RPDITDTEME TVMDTIVDSL FCFVTLGAV PIIRCSRGTA AEMVAVKLDK KLRENLRDAR240  
 NSLFTGDTLG AGQFSFQRPL LVLVDRNIDL ATPLHHTWTY QALVHDVLDL HLNRVNLEES300  
 SGVENSPAGA RPKRKNKKS YDLTPVDKFWQ KHKGSPFPEV AESVQQUELES YRAQEDEVKR360  
 LKSIMGLEGE DEGAISMLSD NTAKLSAVS SLPELLEKKR LIDLHTNVAT AVLEHIKARK420  
 LDVYFEYEEK IMSKTTLDKS LLDIISDPDA GTPEDKMRLF LIYYISTQQA PSEADLEQYK480  
 KALTDAGCNL NPLQYIKQWK AFTKMASAPA SYGSTTTKPM GLLSRVMNTG SQFVMEGVKN540  
 LVLKQONLPV TRILDNLMM KSNPETDDYR YFDPKMLRGN DSSVPRNKNP FQEAIVFVVG600  
 GGNIEYQNL VDYIKGKQK HILYGCSELF NATQFIKQLS QLGQK 645

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 101 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGPSQLRLH YPRISMAVRQ WVIALALAA LVVDREVPVA AGKLPFSRMP ICEHMOVESPT 60  
 CSQMSNLVCG TDGLTYTNEC QLCLARIKTK QDIQIMKDGK C 101

## (2) INFORMATION ON SEQ ID NO. 218:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

QLGWIFYFMS YPLHAHHCSP ADTSWLEVLL WDOHLPSFMI WMSCLVFIRA KQSWHSFVYV 60  
 SPSVPQTRL D IWEQVG DSTM CSQM GILEKG SFPAATGTSL STTRRAAKAR AITHWRTAML120  
 ILG 123

## (2) INFORMATION ON SEQ ID NO. 219:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 64 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

IKAKENLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVL SIVRGIQ PEIKPIYKHV60  
 CSSK 64

## (2) INFORMATION ON SEQ ID NO. 220:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 67 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

SFAIPFPWHC TISPIIGQSL GFLGFTMVAT TIRLIDGSNL KKKVMVMDKI SRSREVCYHK60  
ITVASTS 67

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

TIISITDSQ LQEVAEQLEI FAALHEVLHI INDRKNLKGQ LQEVAEQLEL ERIGPQHQAQ 60  
SDSLLTGMAF FKMREMFED HIDDAKYCGH LYGLGSGSSY VQNGTGNAEY EEANKQS 117

(2) INFORMATION ON SEQ ID NO. 222:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 196 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

PTCPIQHFM MKLWVPSRSL PNSPNHYRSF LSHTLHIRYN NSLFISNTHL SRRKLRVTNP 60  
IYTRKRSINI FYLLIPSCRT RLILWIIYIY RNLKHWSTST VRSHSHSIYR LRPSMRTNII120  
LRCHSYKPP ISHPYWNPN SRMNLRLLS RQSHLDPIR FPLHLTIYYR GPSNRSPPLP180  
PRNRKQPNR IKLRCR 196

## (2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 174 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

LPSAIEGPTP VSALLHSSTI VVAGIFLLVR FHPLTTNNNF ILTTILCLGA LTTLFTAICA 60  
 LTQNDIKKII AFSTSSQLGL IIVTLGINQP HLAFLHICHT AFFKAILFIC SGSIHSLAD120  
 EQDIRKIGNI TKIIPFTSSC LVIGSLALTG IPFLTGFYSK DLIEAINTC NTNA 174

## (2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

FLKTTALIIS VLGFLIALEL NNLTIKLSIN KANPYSSFST LLGFFPSIIH RITPIKSLNL 60  
 SLKTSLTLLD LIWLEKTIPK STSTLHTNIT TLTTNQKGLI KLYFISFLIN IILIIILYSI120  
 NLE 123

## (2) INFORMATION ON SEQ ID NO. 225:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 129 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

NMLLAEVRI\$ MVIRNSVRYL MNRLMEGSEC IYHEENCIID HVTKRATDVN RIEKKSVLKL 60  
 ILSSIEFMVT QCQVVIYYSI LLWKNINRGK RLIMKENLID VVVYSGKLMC LIRFDIEIRI120  
 GDSRRMKIK 129

(2) INFORMATION ON SEQ ID NO. 226:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

FFFFFFFAIQ MNVYFLNPHR VRAELRDAWH SISHPGSLPR SFFFAGSILD LYHFLQRQYP60  
 EWQSQVYFKV GVFSGSRGDW IPS 83

(2) INFORMATION ON SEQ ID NO. 227:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

SMMLEFKVLVI TVFCGLTVAF PLSELVSINK ELQNSIIDLL NSVFDQLGSY RGTKAPLEDY 60  
 TDDDLSTDSE QIMDFTPAAN KQNSEFSTDV ETVSSGFLEE FTENTDITVK IPLAGNPVSP120  
 TS 122

(2) INFORMATION ON SEQ ID NO. 228:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 62 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

TSTTVFFFPF HSLPVGCTV CSHALCINIL EIYRSVLYFL YCWILIIKTF TRVLNKSSLT60  
 RK 62

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 99 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ARPCMNSTKA LPHGREHTRL KMLSYLKNKM CKSSGWHKTK VNASWGTFRL GLAECVNIID60  
 FCLCYMTSVT SLKICTIQFQ LWITSVDLCE GFYLCRMGV 99

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GELQKSSHYH PPELFEMIFF VHFGCSIGGR IYYNMDHLYF CIYLFITRPQ PQSSFSPSTS60  
LCL 63

(2) INFORMATION ON SEQ ID NO. 231:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 64 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

INKYRSRDDP YYSIFYHQYC SQNVQKKSFQ ITQEDDNGWT FVIHLKDCGR ANSTHCIVCA60  
YGGL 64

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 88 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

PLFCAILKTC TFYFSDSLTF LIECVLYHAV MLWYYSYRVL PILKTCHFPK RSFDSALEVEL60  
HKLKSLSNIN MKGGTGCONIY SQVTSLYI 88

## (2) INFORMATION ON SEQ ID NO. 233:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 161 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```

ASTIMDLLFG RRTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIID IKKMAKQGQM 60
DAVRIMAKDL VRTRYVRKF VLMRANIQAV SLKIQTLKSN NSMAQAMKGV TKAMGTMNRQ120
LKLPIQKIM MEFERQAEIM DMKEERIELL HLMIPWVLGK F 161
  
```

## (2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 120 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

RRVRTKSFAM MRTASIWPCL AIFLMSAMIF FSWVSSFCRS RSSSRMARFR ALWFCRSSSS 60
GVFRRPNNRS MMVEAHWQAG AGTDTRFRFR VTLLFLGSPT CPPTKAPRSC RRRRRFRGRV120
  
```

## (2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

KLPQNPRDHQ MQQFNPLLLH IHDLCPLKLL HHDLLDLGQL QLSVHGAGHL GDTLHGLCHR 60  
VVGLECLDLE GHSLDVGPHQ YKLAHIAPGA HQVFCHDANS IHLALLGHLL NVCNDFLLLG120  
L 121

(2) INFORMATION ON SEQ ID NO. 236:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 180 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

KTKRSVKDAA KKGQKDVCI V LAKEMIRSRK AVSKLYASKA HMNSVLMGMK NQLAVLRVAG 60  
SLQKSTEVMMK AMQSLVKIPE IQATMRELSK EMMKAGIIEE MLEDTFESMD DQEEMEEAE120  
MEIDRILFEI TAGALGKAPS KVTDALPEPE PPGAMAASED EGEEEEEALAE MQSRLATLRS180

(2) INFORMATION ON SEQ ID NO. 237:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 111 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

LMPFQSQNLQ ERWLPQRMRG RKRKLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60  
ALHLCCEDYH FGEGSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRKKKKK K 111

## (2) INFORMATION ON SEQ ID NO. 238:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 103 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

KICERCCQEG PEGCLHSSGQ GDDQVKEGCE QAVCIQSTHE LSAHGDEEPA RGLASGWFFA 60  
 EEHRSDGEGA KSCEDSRDSG HHEGVVQRND EGWDHRGDVR GHF 103

## (2) INFORMATION ON SEQ ID NO. 239:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 351 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

TWCTTTMLAA RLVCLRTLPS RVFHPAFTKA SPVVKNSITK NQWLLTPSRE YATKTRIGIR 60  
 RGRTGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120  
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180  
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240  
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFMFLLYD300  
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

## (2) INFORMATION ON SEQ ID NO. 240:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein

(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

RVAPATVVGG RNIDPNEDTK TRPRPTPRGA PMFRNFSLGA HMATVERPPT MPAVYHAALM 60  
RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120  
MKFMRTGVLL IAMADKAVKP ILPAKYI 147

(2) INFORMATION ON SEQ ID NO. 241:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 196 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

KARRRGTMMAA AADERSPEDG EDEEEEEQLV LVELSGIIDS DFLSKCENKC KVLGIDTERP 60  
ILQVDSCVFA GEYEDTLGTC VIFEENVEHA DTEGNNKTVL KYKCHTMKKL SMTRTLTEK120  
KEGEENIGGV EWLQIKDNDF SYRPNMICNF LHENEDEEVV ASAPDKSLEL EEEEIQMNR180  
FKPGFVEPGE PIAPWE 196

(2) INFORMATION ON SEQ ID NO. 242:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 156 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PPAPALRHRE TRRPVASLHV GTGALGARSH PPAGSRHLEF WQKQFARRGA DGQEPNKLLR 60  
 LGAEARTQDG GSGRAWPVTR RRGAGPWRR RRTSGVQRTE KTRKRRSSWF WWNYQELLIQ120  
 TSSQNVKINA RFWALTLRGP FCKWTAVSLL GSMKTL 156

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

RRLEVSyrQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEVQSL 60  
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120  
 PELDGKTAKM YR 132

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 159 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

LFAISYSVLP VHLCCLSIQL RNCNFWGSSR ICDRNVKLDV KLIFQEVMDI PAFSKPPSSF 60  
 LVGLQSEPIV VSILVVLHIP DKGLIFLLQS LHPQLTISGS GVSLQHRDLR HNTSRGFIRH120  
 LGPGRKRNAE VVLPVAYLKA PSSLLWEDET LGCKTSFE 159



## (2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 103 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATLPDALPPA TKFFLKAFDD SLPSPIQSYL YIFAVFPSSS GTAISGAVVG YVIGMSNSMS 60  
 NSYFRRSWIY QHFPNHRVPS LLDSSRNQSL SAFLLFSTYR IRD 103

## (2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 285 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60  
 SPFHDIPIYA DKDVFHVMVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120  
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180  
 GETDWKVIAl NVDDPDAAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240  
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKR IMLIVQLFVG PLKVC 285

## (2) INFORMATION ON SEQ ID NO. 247:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 94 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TKGLRIAQAQ LCPGSPRCRS QSISRACAL CLRPTQPNT TYLRKPGGRK RAVGHKSPAE60  
TRVPASVQRS QPPRAHRKSC LASLGLCKNN KCLS 94

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 113 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

DPRPSRIQHI SGNPAGASER LAIRAQLKRE YLLQYNDPNR RGLIENPALL RWAYARTINV 60  
YPNFRPTPKN SLMGALCGFG PLIFIYYIHK TERDRKEKLI QEGKLDRTFH LSY 113

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 98 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

VFRSGSEIRI DIYCSCIGPT KQGRIFDEPS AVGIVVLKQV LSFQLGSYGQ PLACARRVSG60  
DMLYSAGSRV SGRVRLDGL YFGNDILANQ GTIAPARF 98

## (2) INFORMATION ON SEQ ID NO. 250:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 158 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TQVMVQSMFA PTDTSDMEAV WKEAKPEDLM DSKLRCVFEL PAENDKPHDV EINKIISTTA 60  
 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVQRLRE ENKQFKEEDG LRMRTVQSN120  
 SPISALAPTG KEEGLSTRLL ALVVLFVIGV VIIGKIAL 158

## (2) INFORMATION ON SEQ ID NO. 251:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 112 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

VNKALPFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDTESSL 60  
 GREWATWGLL CGADRTPOHA GLQLPKGQHQ QARKGVILRE VIQHHVPRPT NV 112

## (2) INFORMATION ON SEQ ID NO. 252:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 135 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

SKGCSITETV TVDPGSIIP LGLTQYRRGA VVFTLKHTFL SDGFRNLRFV VTTSVKGPLN 60  
 LRSVGGSRTR ICSSSPWPLR RTPSERQRR GGGLLAGGGG RWREGRGSEF ASLLFLVRLC120  
 STTFLCWQIC FQIDF 135

- (2) INFORMATION ON SEQ ID NO. 253:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 189 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

SMQSAVSFFF FSLDQKKICL PTISLVVWPT VTIFLCVQRH IGFAFNDLLR LENTIKTNCS 60  
 ATGQVVYYQI ITSRCQLHIE SPMKFINKEL FFLCGFNKSS RIVQSLVNVI LIIPLNFIICC120  
 CYLLKYDLFR LLIPLIQEMP RGIPWGN GAS YSVNFSSFTF ANIMAEFFLS LVRQLLTEFF180  
 ILTILSHGI 189

- (2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 300 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

KSIWKQICQH KNVVEQSLTR KRRDANS LPL PSRHRPPPPA SKPPPALRCL SDGVRLRGHG 60  
 EDEQILVLDL PTDLKFKGPF TDVVTNLKL RNPDRKVCF KVKTTAPRRY CVRPNSGIID120  
 PGSTVTVSVM LQPFDYDPNE KSKHKFMVQT IFAPPNTSDM EAVWKEAKPD ELMSKLRVCV180  
 FEMPENNDKL NDMEPSKAVP LNASKQDGPM PKPHSVSLND TETRKLMEEC KRLQGEMMKL240  
 SEENRHLRDE GLRLRKVAHS DKPGSTSTAS FRDNVTSPLP SLLVVIAAIF IGFFLGKFIL300

## (2) INFORMATION ON SEQ ID NO. 255:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGSGS 60  
 HNWGTVKDEL TESPKEYIQKQ ISYNYSDLQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120  
 EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EAHAEVSVMD180  
 HHFRKPANDI TSQLEINFGD LGRPGRGGR GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240  
 EAFPALA 247

## (2) INFORMATION ON SEQ ID NO. 256:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 69 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

FVFDSSPVVR SATSTFVLVL QARSITSTMP IKFTFATRIK SISSAHSTST APSTLFQDHH60  
 DLESRAARA 69

## (2) INFORMATION ON SEQ ID NO. 257:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 220 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```
PGRGSMYDRM RRGGDGYDGG YGGFDDYGGY NNYGYGNDGF DDRMRDGRGM GGHGYGGAGD 60
ASSGFHGGHF VHMRLPFR TENDIANFFS PLNPIRVHID IGADGRATGE ADVEFVTHED120
AVAAMSKDKN NMQHRYIELF LNSTPGGSG MGGSGMGGYG RDGMDNQGGY GSVGRMGGMGN180
NYSGGYGTPD GLGGYGRGGG GSGGYGQGG MSGGGWRGMY                      220
```

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1105 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AATGAGCCTG GTGTTAGATG AGTTTTACAG CTCACTCAGG GTGGTGGGTG TCTCTGCTGT 60
TCTGGGTACT GGATTAGATG AACTCTTTGT GCAAGTTACC AGTGCTGCCG AAGAATATGA 120
AAGGGAGTAT CGTCCTGAAT ATGAACGTCT GAAAAAATCA CTGGCCAACG CAGAGAGCCA 180
ACAGCAGAGA GAACAACTGG AACGCCTTCG AAAAGATATG GGTTCGTAG CCTTGGATGC 240
AGGGACTCCC AAAGACAGCT TATCTCCTGT GCTGCACCC TCTGATTGA TCCTGACTCG 300
ACCAACATTG GAAGCAGACA GCGATACTGA TGACATTGAC CACAGAGTTA CAGAGGAAAG 360
CCATGAAGAG CCAGCATTCC AGAATTTTAT GCAAGAATCG ATGGCACAAT ACTGGAAGAG 420
AAACAATAAA TAGGAGACTT TAGCACACTT CACTTGTTTC TAGAAGTCCA GAATTTTGGA 480
CCTCCACGTG AAAGAAGTGT TCTTACCTCT GAACTGGGGG CTCCCATAAG GGATAATTTT 540
CCTCAGAGTA GCAAAGTTTC TCTTATTAGA GAAATCTTGT GACTCAGATG AAGTCAGGGA 600
TAGAAGACCC TTGGACCTGG CAGGTTAATG CTGATTATTC CTTGGCCTTT CCCTTGATT 660
TATGCAAGGA AGGATATACT GAGCTGATAC TCTTCCAAGC CTACAACTTC AAGTTTTATC 720
ATTTGAACTC AAGTACTTTT GCTGCTGAGG AATGGAATCA AAAGAACGTA GTCTCCTGGT 780
AACCACCTCA GATCTCTATT ATTAGGCTAG ATGTATAGCC TCTACTCCCC CAGCTTCTTG 840
CTCTTGACCC TGCACTGTAA GTTGCCCTTC TATTAGCAGC CAAGGAAAAG GGAAACATGA 900
GCTTATCCAG AACGGTGGCA GAGTCTCCTT GGCAATCAAC CAACGTTGCT ATGAAATATG 960
CCTCACACTG TATAGCTCAT TATAGGACGT CAGGTTTGTT GAAAAAAGTG GGCAAGACAT1020
GATTAATGAA TCAGAATCCT GTTTCATTGG TGAATTGGAT AAAGACTTTT TAATTTTAAA1080
AAAAAAAAA AAAAAAAAAA AAAAA                      1105
```

## (2) INFORMATION ON SEQ ID NO. 259:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1088 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

```

ATTCCAAACA TGGCGGCTCC ACTAGGGGGT ATGTTTTCTG GGCAGCCACC CGGTCCCCCT 60
CAGGCCCCGC CGGGCCTTCC GGGCCAAGCT TCGCTTCTTC AGGCAGCTCC AGGCGCTCCT 120
AGACCTTCCA GCAGTACTTT GGTGGACGAG TTGGAGTCAT CTTTCGAGGC TTGCTTTGCA 180
TCTCTGGTGA GTCAGGACTA TGTCAATGGC ACCGATCAGG AAGAAATTCG AACCGGTGTT 240
GATCAGTGTA TCCAGAAGTT TCTGGATATT GCAAGACAGA CAGAATGTTT TTTCTTACAA 300
AAAAGATTGC AGTTATCTGT CCAGAAACCA GAGCAAGTTA TCAAAGAGGA TGTGTCAGAA 360
CTAAGGAATG AATTACAGCG GAAAGATGCA CTAGTCCAGA AGCACTTGAC AAAGCTGAGG 420
CATTGGCAGC AGGTGCTGGA GGACATCAAC GTGCAGCACA AAAAGCCCGC CGACATCCCT 480
CAGGGCTCCT TGGCCTACCT GGAGCAGGCA TCTGCCAACA TCCCTGCACC TCTGAAGCCA 540
ACGTGAGCAA AGGGCAGAGG CAGTTGGCCT ATGAGTGGGC TGATGCGTGA GGTGGCCAC 600
ACATTCCTTC CTGTGGACTT GACATTTTGG AAGAACTCTT TGCCAGATAA TGAGTTCATT 660
TTAGTTTAT GCTCCCATG AAAAATTTTC CACTATTTT ATAAGCTGTT AATTTCTTGA 720
GTACTTTATA ACATGTCTGT AGCTTGATA AACCAAGTAA GTATTTTTT TTTGCTTTA 780
GCCAAGTTTA GACTGTGAAT ATGATGACAC AGATTCCTTT TTATGGTGGC TTTGCTTGT 840
TTAAATTTT GCATGACTTT TCATCTTTT ATGTGTGTTT CCTGTAGTTT GATCCGAAG 900
AAAAGAGTAT AGTAGCCTGA GAATCAGGAG ATGGGAGTTT TAGTCGTAGG CCTTATGATA 960
ATTACCCCGC GGTGGTGTGT AGAAAAGTAT GTAAATTTGC TCTGTTTTAA GACTTTGAAC 1020
TACCTCAAGA AGAGGAATCT AATACAATAT TTGTAATGTT AAAAAAAAAA AAAAAAAAAA 1080
AAAAAAAAA                                     1088

```

## (2) INFORMATION ON SEQ ID NO. 260:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3292 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
  - (A) ORGANISM: HUMAN
  - (C) ORGAN:
- (vii) OTHER ORIGIN:
  - (A) LIBRARY: cDNA library



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

```

ATGCCGAAC TCTGCGCTGC CCCCACCTGC ACGCGGAAGA GCACGCAGTC CGACTTGGCC 60
TTCTTCAGGT TCCCGCGGGA CCCTGCCAGA TGCCAGAAGT GGGTGGAGAA CTGTAGGAGA 120
GCAGACTTAG AAGATAAAAC ACCTGATCAG CTAAATAAAC ATTATCGATT ATGTGCCAAA 180
CATTTTGAGA CCTCTATGAT CTGTAGAACT AGTCCTTATA GGACAGTTCT TCGAGATAAT 240
GCAATACCAA CAATATTTGA TCTTACCAGT CATTTGAACA ACCCACATAG TAGACACAGA 300
AAACGAATAA AAGAAGTGAAG TGAAGATGAA ATCAGGACAC TGAACAGAA AAAAATTGAT 360
GAAACTTCTG AGCAGGAACA AAAACATAAA GAAACCAACA ATAGCAATGC TCAGAACCCC 420
AGCGAAGAAG AGGGTGAAGG GCAAGATGAG GACATTTTAC CTCTAACCCCT TGAAGAGAAG 480
GAAAACAAAG AATACCTAAA ATCTCTATTT GAAATCTTGA TTCTGATGGG AAAGCAAAAC 540
ATACCTCTGG ATGGACATGA GGCTGATGAA ATCCCAGAAG GTCTCTTTAC TCCAGATAAC 600
TTTCAGGCAC TGCTGGAGTG TCGGATAAAT TCTGGTGAAG AGGTCTGAG AAAGCGGTTT 660
GAGACAACAG CAGTTAACAC GTTGTTTTGT TCAAAAACAG AGCAGAGGCA GATGCTAGAG 720
ATCTGTGAGA GCTGTATTCT AGAAGAAACT CTCAGGGAAG TGAGAGACTC ACACCTCTTT 780
TCCATTATCA CTGACGATGT AGTGGACATA GCAGGGGAAG AGCACCTACC TGTGTTGGTG 840
AGGTTTGTGT ATGAATCTCA TAACCTAAGA GAGGAATTTA TAGGCTTCCT GCCTTATGAA 900
GCCGATGCAG AAATTTTGGC TGTGAAATTT CACACTATGA TAACTGAGAA GTGGGGATTA 960
AATATGGAGT ATTGTCGTGG CCAGGCTTAC ATTGTCTCTA GTGGATTTTC TTCCAAAATG1020
AAAGTTGTTG CTTCTAGACT TTTAGAGAAA TATCCCAAG CTATCTACAC ACTCTGCTCT1080
TCCTGTGCCT TAAATATGTG GTTGGCAAAA TCAGTACCTG TTATGGGAGT ATCTGTTGCA1140
TTAGGAACAA TTGAGGAAGT TTGTTCTTTT TTCCATCNGA TCACCACAAC TGCTTTTAGA1200
ACTTGACAAC GTAATTGCTG TTCTTTTTC GAACAGTAAA GAAAGGGGTA AAGAACTGAA1260
GGAAATCTGC CATTTCTCAGT GGACAGGCAG GCATGATGCT TTTGAAATTT TAGTGGAACT1320
CCTGCAAGCA CTTGTTTTAT GTTTAGATGG TATAAATAGT GACACAAATA TTAGNATGGG1380
AATAACTATA TAGCTGGCCG AGCATTNGT ACTCTGCAGT GCAGTGCAG ATTTTGATTT1440
CATTGTTACT ATTGTTGTTT TAAAAATGT CCTATCTTTT ACAAGAGCCT TTGGGAAAAA1500
CCTNCCANGG GGCAAACTC GTGATGCTT CTTTGCGGCC GGTAGCTTGA CTNGCAGTAC1560
TGNNCATTCA CNTCAACGAA GTGAGTGGGA AAATATTNGA AGTTTATCAT GAATTTTGGT1620
TTGAGGAAGC CACAAATTTG GCAACCAAC TTGATATTCA AATGAACTC CCTGGGAAAT1680
TCCGAGAGC TCACCNAGG GTAACCTGGA ATCTCAGCTA ACNCTCTGAG AGTTACTATA1740
AAGAAACCCN TAAGTGTCCT AACAGTGGAG CACATTATTC AGGAACTTAA AGATATATTC1800
TCAGAACAGC ACCTCAAAGC TCTTAAATGC TTATCTCTGG TACCCTCAGT CATGGGACAA1860
CTCAAATTC AATACGNTCNG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA1920
ATCCTGACAC GCTGTCAGT GAGCTTCATT GTTGGAGAA CAAATGGAAA CACAGGGGGA1980
AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT2040
TTCCTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA2100
ATGAGCGGTA TGAAAAATG ACGAAAGCGT CTTTAAAGCA TATTTGAGGG AACACTTTGA2160
CAGACCCAAA GGTCAAGTAA CTTGGCTTTT GCTTTAACAT AAATTTTGA TATTAAACA2220
CGACCTGGAT TTAATGGTGG ACACATATAT TAACTCTAT ACAAGTAACT CAGAGCTTCC2280
TACAGATAAT TCCGAACTG TGGNAAAATA CCTAAGAGAC TTTTAAAAAT AGGCTTTCTT2340
ATATTTGATA TTTGGAAGAA AAAGCCGTAA GGTGTATGTA GACCACTTAA TCACTAAATA2400
TCTTTGCCTA TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG2460
CCCCTGTTTG AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA2520
AGTGCCATGT TTCCNTTTTG CGTGATCTCT GTTGATGGCA CTCTGGAATT GTTTCAGTTA2580
AGTCATTTTA GACATAGCAT TTATTATCAC TGTGGNATCT CTACTTGTG GGTGTTATGA2640
ATTCTTTGNA AGNAAATATA TTTTNGAAGA GGTGTGGGNA GGNAAGGAAT ACNATTTTAT2700
NAAAATGTTG TAGTGNAAGN CCCACAATTN GACCTTTNGA CTAATANGGA GTTTTAAGTA2760
TNGTTAAAAA TNCTATACTG GNNACAGNTT ACAAGAAATT ACCGGAGAAA AGCTTGTGAG2820
CTCACCNAAA CAAGGNATTT NCAGTGTAGA TTTTGTCTNT TCTTGAACNT TNAAGAAAN2880
CAATGANCA AAGTTTGAAT NGGAAAAGCC TGCTGTTGTT CCNACATCTC NGTTGCTGTT2940
NNTACANTTC CNNTTTTGTG GAGNCCTACN ATCTTNCCTA AGCTTTTNA GCANGGTATA3000

TNGTTGAACA CTTCTNGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAAC3060
TGATTTGTCT GTTTTTTTTC TCTGTCTTIN TTCCATGACT CTTATATACT GCCTCATCTT3120
GATTTATAAG CNAAAAACCT GGANAAACCT ANCAAAATAA GTGTTGTGGT TTATCTAGAA3180
AAATATGGAA AATATTGCTG TTATTTTGG TGAAGAAAAT CNAATTTTGT ATAGTTTATT3240
TCAATCTAAA TAAAATGTGA ATTTTGTTTA AAAAAAAAAA AAAAAAAAAA AA 3292

```

## (2) INFORMATION ON SEQ ID NO. 261:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1196 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```

GGTAGAAAT  GCAATAAAT  CTGGGACAAT  GCCCAGACCT  CTGGCATAGA  GGAGCCTTCT  60
GAGACAAAGG  GTTCTATGCA  AAAAAGCAAA  TTCAAATATA  AGTTGGTTCC  TGAAGAAGAA  120
ACCACTGCCT  CAGAAAATAC  AGAGATAACC  TCTGAAAGGC  AGAAAGAGGG  CATCAAATTA  180
ACAATCAGGA  TATCAAGTCG  GAAAAAGAAG  CCCGATTCTC  CCCCCAAAGT  TCTAGAACCA  240
GAAAACAAGC  AAGAGAAGAC  AGAAAAGGAA  GAGGAGAAAA  CAAATGTGGG  TCGTACTTTA  300
AGAAGATCTC  CAAGAATATC  TAGACCCACT  GCAAAAGTGG  CTGAGATCAG  AGATCAGAAA  360
GCTGATAAAA  AAAGAGGGGA  AGGAGAAGAT  GAGGTGGAAG  AAGAGTCAAC  AGCTTTGCAA  420
AAAAGTACA  AAAAGGAAAT  TTTGAAAAA  TCAGAGAAAG  ATACAAATTC  TAAAGTAAGC  480
AAGGTAAAC  CCAAAGGCAA  AGTTCGATGG  ACTGGTTCTC  GGACACGTGG  CAGATGGAAA  540
TATTCCAGCA  ATGATGAAAG  TGAAGGGTCT  GGCAGTGAAA  AATCATCTGC  AGCTTCAGAA  600
GAGGAGGAAG  AAAAGGAAAG  TGAAGAAGCC  ATCCTAGCAG  ATGATGATGA  ACCATGCAAA  660
AAATGTGGCC  TTCCAAACCA  TCCTGAGCTA  ATTCTTCTGT  GTGACTCTTG  CGATAGTGGA  720
TACCATACTG  CCTGCCTTCG  CCCTCCTCTG  ATGATCATCC  CAGATGGAGA  ATGGTTCTGC  780
CCACCTTGCC  AACATAAACT  GCTCTGTGAA  AAATTAGAGG  AACAGTTGCA  GGATTGGAAT  840
GTTGCCTTAA  AGAAGAAAGA  GCGTGCCGAA  CGAAGAAAAG  AACGCTTGGT  GTATGTTGGT  900
ATCAGTATTG  AAAACATCAT  TCCTCCACAA  GAGCCAGACT  TTTCTGAAGA  TCAAGAAGAA  960
AAGAAAAAAG  ATTCAAAAAA  ATCCAAAGCA  AACTTGCTTG  AAAGGAGGTC  AACAGAACA1020
AGGAAATGTA  TAAGCTACAG  ATTTGATGAG  TTTGATGAAG  CAATTGATGA  AGCTATTGAA1080
GATGACATCA  AAGAAGCCGA  TGGAGGAGGA  GTTGGCCGAG  GAAAAGATAT  CTCCACCATC1140
ACAGGTCATC  GTGGGAAAGA  CATCTCTACT  ATTTTGATG  AAAAAATAAT  AACGGC      1196

```

## (2) INFORMATION ON SEQ ID NO. 262:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```

AAGGACGCTT GCCTTTTTC GGTGCGGGAA GGGGGAAGAA GGTAACCTCC GGTGACGGGG 60
TTGCATCACT TCCTCTCAAG CTGCGGCGTT TGTGTTGGTG GGTTACACGC GGGTTCAACA 120
TGCGTATCGA AAAGTGTTAT TTCTGTTCCG GGGCCATCTA TCCTGGACAC GGCATGATGT 180
TCGTCCGCAA CGATTGCAAG GTGTTGAGAT TTTGCAAATC TAAATGTCAT AAAAAGCTTTA 240
AAAAGAAGCG CAATCCTCGC AAAGTTAGGT GGACCAAAGC ATTCCGGAAA GCAGCTGGTA 300
AAGAGCTTAC AGTGGATAAT TCATTTGAAT TTGAAAAACG TAGAAATGAA CCTATCAAAT 360
ACCAGCGAGA GCTATGGAAT AAACTATTG ATGCGATGAA GAGAGTTGAA GAAATCAAAC 420
AGAAGCGCCA AGCTAAATTT ATAATGAACA GATTGAAGAA AAATAAAGAG CTACAGAAAG 480
TTCAGGATAT CAAAGAAGTC AAGCAAAACA TCCATCTTAT CCGAGCCCTT CTTGCAGGCA 540
AAGGGAAACA GTTGAAGAG AAAATGGTAC AGCAGTTACA AGAGGATGTG GACATGGAAG 600
ATGCTCCTTA AAAATCTCTG TAACCATTTT TTTTATGTAC ATTTGAAAAT GCCCTTTGGA 660
TACTTGGAAC TGCTAAATTA TTTTATTTT TACATAAGGT CACTTAAATG AAAAGCGATT 720
AAAAGACATC TTTCTGTCAT TGCCATCTAC ATAATATCAG ATATTACGGA TGTTAGATTG 780
CATCTCAGTG TTAATCTTT ACTGATAGAT GTACTTAAGT AAATCATGAA AATTCTACTT 840
GTAACATAG AAGTGAATTG TGGACGTAAA ATGTTGTGTC TATTTGGATA ATGGCACTAG 900
GCAGCATTTG TATAGTAACT AATGGCAAAA ATTCATGGCT AGTGATGTAT AAAATAAAAT 960
ATTCTTTGCA GTAAAATATT CCCTTTGTTA ATGTTATAGA AGGGGGGATA CAAAAGGAA1020
CTAACAATTT GTATGGCAGT GTCAGATATT TTTATTTTAG TATTCCTGT TTTGGTTTAT1080
TTGCATCTTA GAAGAGCATA ATGACATTGT TTGATGAAGC CTAATTATGC TGGACTGTTT1140
TGACCTGGTT TAACCTTCT GATAGGTAGT TGTGGATGCT GGGGATGAGA ACTGAATAAT1200
CTTTGCCTGG AGTGACACTA CACTCTAGAA TTTCCACTTT GGAGAATACT CAGTTCCAAC1260
TTGTGATTCC TGATAGAACA GACTTTACTT TTCTAGCCCA GCATTGATCT AGAAGCAGAG1320
GAATCCAGC GCCTTTTAAA AGTTGTTATG TGTTTTTCTT TAAAAAGCT CCTGTTTTTG1380
GAAAGTAGAA TTTATGGGTA CAACGTATGT TCATTATTG TACATAAAAT AAAACCATTT1440
AAAAAGTAAA AAAAAAAAAA AAAAAAC
1467

```

(2) INFORMATION ON SEQ ID NO. 263:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 739 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

CGGCTCGAGC CCCGCTCAGT CACCCGCAGC AGGCGTGCAG TTTCCCGGCT CTCCGCGCGG 60
CCGGGGAAGG TCAGCGCCGT AATGGCGTTC TTGGCGTCGG GACCCTACCT GACCCATCAG120
CAAAAGGTGT TCGGGCTTTA TAAGCGGGCG CTACGCCACC TCGAGTCGTG GTGCGTCCAG180
AGAGACAAAT ACCGATACTT TGCTTGTTTG ATGAGAGCCC GGTTTGAAGA ACATAAGAAT240
GAAAAGGATA TGGCGAAGGC CACCCAGCTG CTGAAGGAGG CCGAGGAAGA ATTCTGGTAC300
CGTCAGCATC CACAGCCATA CATCTTCCCT GACTCTCCTG GGGGCACCTC CTATGAGAGA360
TACGATTGCT ACAAGGTCCC AGAATGGTGC TTAGATGACT GGCATCCTTC TGAGAAGGCA420
ATGTATCCTG ATTACTTTGC CAAGAGAGAA CAGTGAAGA AACTGCGGAG GGAAAGCTGG480
GAACGAGAGG TTAAGCAGCT GCAGGAGGAA ACGCCACCTG GTGGTCCTTT AACTGAAGCT540
TTGCCCCCTG CCCGAAAGGA AGGTGATTG CCCCCACTGT GGTGGTATAT TGTGACCAGA600
CCCCGGGAGC GGCCCATGTA GAAAGAGAGA GACCTCATCT TTCATGCTTG CAAGTGAAAT660
ATGTTACAGA ACATGCACTT GCCCTAATAA AAAATCAGTG AAATGAAAAA AAAAAAAA720
AAAAAAAAA AAAAAAAAAA

```

739

(2) INFORMATION ON SEQ ID NO. 264:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2146 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

TTTTTTTTTT	TTTTTTTTTT	TCCCAGGCC	TCTTTTTATT	TACAGTGATA	CCAAACCATC	60
CACCTGCAAA	TTCTTTGGTC	TCCCATCAGC	TGGAATTAAG	TAGGTACTGT	GTATCTTGA	120
GATCATGTAT	TTGTCTCCAC	CTTGGTGGAT	ACAAGAAAGG	AAGGCACGAA	CAGCTGAAA	180
AGAAGGGTAT	CACACCGCTC	CAGCTGGAAT	CCAGCAGGAA	CCTCTGAGCA	TGCCACAGCT	240
GAACACTTAA	AAGAGGAAAG	AAGGCAGCT	GCCTCTTATT	TATTTTGAAA	GCAAATTCAT	300
TTGAAAGTGC	ATAAATGGTC	ATCATAAGTC	AAACGTATCA	ATTAGACCTT	CAACCTTAGGC	360
TATTTAATAA	TACACCACAC	TGAAATTATT	TGCCAATGAA	TCCCAAAGAT	TTGGTACAAA	420
TAGTACAATT	CGTATTTGCT	TTCTCTTTTC	CTTCTCTCAG	ACAAACACCA	AATAAAATGC	480
AGGTGAAAGA	GATGAACCCAC	GACTAGAGGC	TGACTTAGAA	ATTTATGCTG	ACTCGATCTA	540
AAAAAAATTA	TGTTGGTTAA	CGTTAACTA	CTTAAATCG	GGCCCTTTCG	GCAAGCCTTT	600
CAAAAGGAGT	CAAGTCACAG	TCATACAGCT	AGAAAAAGTC	CTGAAAAAAA	GAATTGTTAA	660
GAAGTATAAT	AACCTTTTCA	AAACCCACAA	CGCAGCTTAG	TTTTCTTTTA	TTTATTTGTG	720
GTCAAGAAGA	CTATCCCAT	TTCTCCATAA	AATCCTCCCT	CCATACTGCT	GCATTATGGC	780
ACAAAGAGCT	CTAAGTGCCA	CCAGACAGAA	GGACCCAGAT	TTCCGATTAT	AAACAATGAT	840
GCTGGGTAAT	GTTTAAATGA	GAACATTGGA	TATGGATGTT	CAGATGAAAG	CTCAGGCCGA	900
ATTCCGCTCG	AGCTTTTCAT	TGACCATCCA	TATCCAATGT	TCTCATTTAA	ACATTACCCA	960
GCATCATTGT	TTATAATCAG	AAACTCTGGT	CCTTCTGTCT	GGTGGCACTT	AGAGTCTTTT	1020
GTGCCATAAT	GCAGCAGTAT	GGAGGGAGGA	TTTTATGGAG	AAATGGGGAT	AGTCTTCAATG	1080
ACCACAAATA	AATAAAGGAA	AACTAAGCTG	CATTGTGGGT	TTTGAAAAAGG	TTATTATACT	1140
TCTTAACAAT	TCTTTTTCCT	GGGACTTTTC	TAGCTGTATG	ACTGTTACTT	AAACTCTCTA	1200
AAATGAGACA	TTTTGGTATC	TTTCATCTGA	CCATCCATAT	CCAATGTTCT	CATTTAAACA	1260
TTACCCAGCA	TCATTGTTTA	TAATCAGAAA	CTCTGGTCTT	TCTGTCTGGT	GGCACTTAGA	1320
GTCTTTTGTG	CCATAATGCA	GCAGTATGGA	GGGAGGATTT	TATGGAGAAA	TGGGGATAGT	1380
CTTTCATGAC	ACAAATAAAT	AAAGGAAAAA	TAAGCTGCAT	TGTGGGTTTT	GAAGAGGTTA	1440
TTATACCTCT	TAAGCAATTCT	TTTTTTCAGG	GACTTTTCTA	CGTGTATGAC	TGTTACTTTGA	1500
CCCTTCTTGA	AAACCAATTC	CAAAATGCTC	TATTTTAGAT	AGATTAACAT	TAAACCAACT	1560
AATTTTTTTT	AGATCGAGTC	AGCATAAATT	TCTAAGTCAG	CCTCTAGTCG	TGGTTCATCT	1620
CTTTCACCTG	CATTTTATTT	GGTGTGTTGC	TGAAGAAAGG	AAAGAGGAAA	GCAAAACGA	1680
ATTGTACTAT	TTGTACCAAA	TCTTTGGGAT	TCATTGGCAA	ATAAATTCAG	TGTGGTGTAT	1740
TATTAATAAT	AAAAAATAAA	TTTTGTTTCC	TAGTTTGAAG	GTCTAATTGA	TACGTTTGAC	1800
TTATGATGAC	CATTTATGCA	CTTTCAAATG	AATTTGCTTT	CAAAATAAAT	GAAGAGCAGC	1860
TGTCCTTCTT	TCCTCTTTTA	AGTGTTCAGC	TGTGGCATGC	TCAGAGGTTT	CTGCTGGATT	1920
CCAGCTGGAG	CGGTGTGATA	CCCTTCTTTT	TCAGCTGTTT	GTGCCTTCTT	TTCTTGATAT	1980
CACCAAGAGT	GAGACAAATA	CATGATCTCA	AAGATACACA	GTACCTACTT	AATTCCAGCT	2040
GATGGGAGAC	CAAGAAGATT	GCAAGTGGAT	GGTTTGGTAT	CACCTGAAAT	AAAAAGAGGG	2100
CCTGGGAATT	CTTGGCAATC	CATCTCTAAA	AAAAAATAAA	AAAAAA		2140

## (2) INFORMATION ON SEQ ID NO. 265:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```

CAAGTAAATG CAGCACTAGT GGGTGGGATT GAGGCTATGC CCTGGTGCAT AAATAGAGAC 60
TCAGCTGTGC TGGCACACTC AGCGGCTCTG GACCGCATCC TAGCCGCCGA CTCACACAAG 120
GCAGGTGGGT GAGGAAATCC AGAGTTGCCA TGGAGAAAAT TCCAGTGTCA GCATTCTTGC 180
TCCTTGTGGC CCTCTCTAC ACTCTGGCCA GAGATACCAC AGTCAAACCT GGAGCCAAAA 240
AGGACACAAA GGAATCTCGA CCCAACTGC CCCAGACCCT CTCCAGAGGT TGGGGTGACC 300
AACTCATCTG GACTCAGACA TATGAAGAAG CTCTATATAA ATCCAAGACA AGCAACAAAC 360
CCTTGATGAT TATTCATCAC TTGGATGAGT GCCCACACAG TCAAGCTTTA AAGAAAGTGT 420
TTGCTGAAAA TAAAGAAATC CAGAAATTGG CAGAGCAGTT TGTCTCCTC AATCTGGTTT 480
ATGAAACAAC TGACAAACAC CTTTCTCCTG ATGGCCAGTA TGCCCCAGG ATTATGTTTG 540
TTGACCCATC TCTGACAGT AGAGCCGATA TCACTGGAAG ATATTCAAAC CGTCTCTATG 600
CTTACGAACC TGCAGATACA GCTCTGTTGC TTGACAACAT GAAGAAAGCT CTCAGTTTGC 660
TGAAGACTGA ATTGTAAAGA AAAAAAATCT CCAAGCCCTT CTGTCTGTCA GGCCTTGAGA 720
CTTGAAACCA GAAGAAGTGT GAGAAGACTG GCTAGTGTGG AAGCATAGTG AACACACTGA 780
TTAGGTTATG GTTTAATGTT ACAACAATA TTTTTAAGA AAAACAAGTT TTAGAAATTT 840
GGTTTCAAGT GTACATGTGT GAAAACAATA TTGTATACTA CCATAGTGAG CCATGATTTT 900
CTAAAAAAA AAATAAATGT TTTGGGGGTG TTCTGTTTTC TCCAAAAAAA AAAAAAAA 960
AAAAAAA AAAAATTGCC CCCAAGGGGA CGGGTTACAA TTGGGGGGCG1020

```

## (2) INFORMATION ON SEQ ID NO. 266:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1652 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

AATTCGGATC CATGGGCCAC AGTGGATGGC TTGAAATGTG GCTGAGCGCT TCGGACAATT 60
CGGATCCATG NNNNGTGGCC ACCCCAAGAC GCGCCCCAGC CCGCCATGGC CCGGATCCTN 120
NCCGGGNNTC CTGCTTCTG TCCCTGCTCC TGGCCGGNGT TTGTTCCGCC GGGCCGGGGA 180
CAAGAGAAGT CTAAGACAGA CTGCCATGGC GGTNATGAGT GGTACCATCT ACGAGTATGG 240
AGCCCTCACC ATCGATGGGG AGGAATACAT TCCTTTTAAG CAGTATGCAG GCAAATATAT 300
CCTCTTTGTC AACGTAGCCA GCTACTGAGG TCTGACAGAC CAATACCTTG AACTGAATGC 360
ACTACAAGAA GAACCTGGGC CATTGGCTN TGGTCATTCT GGGCTTCCCT TCCAACCAAT 420
TTGGCAAACA GGAGCCAGGC GAGAAGTCGG AGATACTCCC CAGTCTCAAG TATGTTTCGNN 480
ACCAGGTNNG GGGGCTTTGT GNCCTAATTN NNNTCCAGNC TCNTTTGAGA AANNNGGANGA 540

TNSTNGAACN GGGGAGNAAA GAGCNAGAAA TTCTACACTT TCCTGAAGAA CTCCTGCCCT 600
CCCACTGCAG NAACTCCTGG GNCTCANCCT GGCCGCNCTC TTTTGGGAAC CCATGAAGAT 660
CCATGACATN CCGCTGGAAC TTTGAGAAGT TCCTGGTNGG GGCCNAGANT GGCATACCGG 720
TTATGCGCTG GTACCACCGG ACCACAGTCN AGCAACGTCN AAGATGGACA TCCTGNTCNT 780
TACATGAGGC GGCAGGCANG CCCTGANGCG CCNAGGGGGN AAGTAACTGA NTGCCCNNNC 840
CACCTTACCC CTACCCCTTG CCCATCATNG CAAGGGCCGA NGGAGGGGCT CTTCNAGGAA 900
GGAAGCCACA TTCCAGTCA TTCTNANCCC CCACCCAGA TTCTCTTNC TTNATTACAT 960
AAAAGACAAG CCNTGGCACA ACTGTGTGTC TGAACCACTG TNGGACACGT GACAATTGTN1020
CCCAGTGTGT GCATGGCTAC ACAGNCCACG TATCTGCCTG CNTTGAAACC CANGGGNATG1080
GTCCATCNTG TNGTTTACGG NCTTGGCACA ACACCCNNTC ATATTTTTTT CAGCNTTTCT1140
GTTCCAAANN TGAGNNCCCA AANNNGGAAAC ACNAANGTTC TNAGSTCCNA ATNGGTTCTG1200
CTCAAANCCN TGANACATNC ATT CNTTGGG GNCCANGCAT CNTCCACAT NGCCCACACN1260
TACACACCAC CNAGCCTCCT TCTTCTTNC CTGNAAGGAC CCNTCCNNNN TGAGCCCCCA1320
AGCCNCATCC CACAGTGCNT CCTGAGACCA GCCAAGACAA CTGTGAGCGC GATGGCCGTG1380
TANCCCCAGG TNCAGGGGNT GGTGTCTCTA TGAAGGANNG GGNNCCCGNA AGCCCTTGTN1440
GGGNCGGNGC CTCCCTGAG CCCNGTCTGT GGTGCCNAGC CCTTAGTGCA TTCAGGCTTA1500
GGCTCCCNAG GCANGGGACA CTACCCCGCG GCCTCTGGAG GACATGCTAT CCTCTCACTC1560
TGTCCACTGG TATCTCAACA CCCCCTCTG CCCAGTAAAG GTCTTTCTGC AGCAAAAAAA1620
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA GG
1652

```

## (2) INFORMATION ON SEQ ID NO. 267:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1409 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

GGAGTGGCCC TCTGTGAGGG GCTCAATGG TTGCAATTCA TGGCGCGTTA CGACTTGGCT 60
CACTTAATCA AATCCCTACC AACTCTAACT TGCCGAAGGA AGAACTTGAC CTCTTGGAGA 120
ACCCCTCGATT GGTTCCTTCTTCCCT GCCATTTAGA TGTTGAAGTA CCCCATGAAG AGCTGCAAAA 180
ATTCTCAAAG GTGGATTACA GGAGGTGGCA GAACAGTTAG AGCTGGAACG GATAGGACCA 240
CAACATCAGG CAGGATCTGA TTCATTGCTC ACAGGAATGG CCTTTTCAA AATGAGAGAA 300
ATGTTCTTTG AAGATCATAT TGATGATGCC AAATATTGTG GTCATTTGTA TGGCCTTGGT 360
TCTGGTTCAT CCTATGTACA GAATGGCACA GGAATGCAT ATGAAGAGGA AGCCAACAAG 420
CAGTCATGAC ATGAAATAGT CCTTTTATTT TTATTTTCGAG CTACACACAT GCTTGTATAT 480
AGGTTTATC TCTGGTTGAA TCCCTCGAAC AATAGACAGT ACCTTTCCCC CCCCTTTCAT 540
GGCCCATTTT ATTGTCTGCC TTTCAGTACT AAGTATGACC GTTCCTATCT CAGATCTTAA 600
TAAAAAGAAA AAAAAAAGC CATTGAGTT AAATTGGCC TTAATTAAAT ATAATTGTTA 660
GCAAGCGTGT GTGACAGAGA GTGGGGAAG CTACATCATT GAATATTTTG ATAACTTTA 720
CCGACTTGAG TTTGGTTTAT TTTCCCTTT TCCTAAATTA ACTAGCACTG ACTGTAATTT 780

ATTTCCCTGT TTCACGTCTC TCCCTTCCAT TCTGCAGGAG TTTTAGCTAT TTGAGATCGT 840
GGACCATCAG TTTTGCACCT TAGAGAGTGT TTCTGACTCT AAACCTGTTT TATCAGAAAA 900
TTTGTTTTTT CTGATCTTA GCTGGAAAA TCTGCCAACT TTACACAGTA TTTACTTGGT 960
TTTGACCCAC AGAATATAGC ACGTTGTGCA AACTGTCGAT TCAGCGAAAC TAAAAAAGA1020
CAAGAACTA CTGAGGAGCT TAGTAACTGC TGTTTCTGTA CGTAGTGTTT AATCTTCAA1080
GCACATCTAG TGTCTGTCAG TTTCTAATTG GCATGTGTAG GCTGCTCTGT GACTGAAGAA1140
TTTTCAAACC AGCTTTACAC CCTTCAGGAA AAATCCCTGT GATTGGATGG TTAATATCTG1200
CCAGGAACTG GTACCCAGAT GTGAAGCACA GTTATTATGA TAGACACTTC CTGAGTGCTA1260
TTGTATCCAC ACCATTACCT TTTTTTTTAA ATTGGAGCCA TCTATGAGCC TGATTGTGGT1320
CGCAACCATT GTAAAACCCA GAAAGCCTAG GGATTGGCCA ATAATTGGGG AAATGGTGCA1380
GTGCCAAGGA AATGGGATGG CAAAAGAAG                                     1409

```



## (2) INFORMATION ON SEQ ID NO. 268:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 900 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

CCCACGCGTC CCGGAAACGG CGGCGGCGGC GACAGGACCG AGGGGCCTTA GTTGGTGGGC 60
AAGTCGGGGA TCCCAGAAAG AGAAGCGTGA CCCGGAAGCG GAAACGGGTG TCCGTCCCAG120
CTCCGGCCTG CCAGTGAGCT TCTACCATCA TGGACCTATT GTTCGGGCGC CGGAAGACGC180
CAGAGGAGCT ACTGCGGCAG AACCAGAGGG CCCTGAACCG TGCCATGCGG GAGCTGGACC240
GCGAGCGACA GAAACTAGAG ACCCAGGAGA AGAAAATCAT TGCAGACATT AAGAAGATGG300
CCAAGCAAGG CCAGATGGAT GCTGTTGCA TCATGGCAA AGACTTGGTG CGCACC CGC360
GCTATGTGCG CAAGTTTGTA TTGATGCGGG CCAACATCCA GGCTGTGTCC CTCAAGATCC420
AGACACTCAA GTCCAACAAC TCGATGGCAC AAGCCATGAA GGGTGTCAAC AAGGCCATGG480
GCACCATGAA CAGACAGCTG AAGTTGCCCC AGATCCAGAA GATCATGATG GAGTTTGAGC540
GGCAGGCAGA GATCATGGAT ATGAAGGAGG AGATGATGAA TGATGCCATT GATGATCCCA600
TGGGTGATGA GGAAGATGAA GAGGAGAGTG ATGCTGTGGT GTCCCAGGTT CTGGATGAGC660
TGGGACTTAG CCTAACAGAT GAGCTGTCGA ACCTCCCCTC AACTGGGGGC TCGCTTAGTG720
TGGCTGCTGG TGGGAAAAAA GCAGAGGCCG CAGCCTCAGC CCTAGCTGAT GCTGATGCAG780
ACCTGGAGGA ACGGCTTAAG AACCTGCGGA GGGACTGAGT GCCCCTGCCA CTCCGAGATA840
ACCAAGTGAT GCCCAGGATC TTTTACCACA ACCCTCTGT AATAAAAGAG ATTTGACACT900

```

## (2) INFORMATION ON SEQ ID NO. 269:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1145 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```

GGGCCCCGCC CAGGCGGCTG CCCGTGACCT GCCTGGGCGC GGGGAAGTGA AAGCCGGAAG 60
GGGCAAGACG GGTTCAAGTC GTCATGGGGC TGTTTGGAAA GACCCAGGAG AAGCCGCCCCA 120
AAGAACTGGT CAATGAGTGG TCATTGAAGA TAAGAAAGGA AATGAGAGTT GTTGACAGGC 180
AAATAAGGGA TATCCAAAGA GAAGAAGAAA AAGTGAACG ATCTGTGAAA GATGCTGCCA 240
AGAAGGGCCA GAAGGATGTC TGCATAGTTC TGGCCAAGGA GATGATCAGG TCAAGGAAGG 300
CTGTGAGCAA GCTGTATGCA TCCAAAGCAC ACATGAACTC AGTGCTCATG GGGATGAAGA 360
ACCAGCTCGC GGTCTTGCGA GTGGCTGGTT CCCTGCAGAA GAGCACAGAA GTGATGAAGG 420
CCATGCAAAG TCTTGTGAAG ATTCCAGAGA TTCAGGCCAC CATGAGGGAG TTGTCCAAAG 480
AAATGATGAA GGCTGGGATC ATAGAGGAGA TGTTAGAGGA CACTTTTGAA AGCATGGACG 540
ATCAGGAAGA AATGGAGGAA GAAGCAGAAA TGGAAATTGA CAGAATTCTC TTTGAAATTA 600
CAGCAGGGGC CTTGGGCAAA GCACCCAGTA AAGTGACTGA TGCCCTTCCA GAGCCAGAAC 660
CTCCAGGAGC GATGGCTGCC TCAGAGGATG AGGGGGAGGA GGAAGAGGCT CTGGAGGCCA 720
TGCAGTCCCG GCTGGCCACA CTCCGCAGCT AGGGGCTGCC TACCCCGCTG GGTGTGCAC 780
CACTCCTCTC AAGAGCTGCC ATTTTATGTG TCTCTTGAC TACACCTCTG TTGTGAGGAC 840
TACCATTTTG GAGAAGGTTT TGTGTGCTC TTTTCATTCT CTGCCAGGT TTTGGGATCG 900
CAAAGGGATT GTTCTTATAA AAGTGGCATA AATAAATGCA TCATTTTATG GAGTATAGAC 960
AGATATATCT TATTGTGGGG AGGGGAAAGA AATCCATCTG CTCATGAAGC ACTTCTGAAA1020
ATATAGGTGA TTGCCTGAAT GTCGAAGACT CTACTTTTGT CTATAAAACA CTATATAAAT1080
GAATTTTAAT AAATTTTTCG TTTAGCACTT GGCCCCATTG TAGATTGCCC TGTGCAGTAA1140
ACTTT
1145

```

(2) INFORMATION ON SEQ ID NO. 270:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1836 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:**

```

GTTGCGACAT GCAGTGCGCC GGAGGAACTG TGCTCTTTGA GGCCGACGCT AGGGGCCCCGG 60
AAGGGAAACT GCGAGGCGAA GGTGACCGGG GACCGAGCAT TTCAGATCTG CTCGGTAGAC 120
CTGGTGCACC ACCACCATGT TGGCTGCAAG GCTGGTGTGT CTCCGGACAC TACCTTCTAG 180
GGTTTTCCAC CCAGCTTTCA CCAAGGCCTC CCCTGTTGTG AAGAATTCCA TCACGAAGAA 240
TCAATGGCTG TTAACACCTA GCAGGGAATA TGCCACCAAA ACAAGAATTG GGATCCGGCG 300
TGGGAGAACT GGCCAAGAAC TCAAAGAGGC AGCATTGGAA CCATCGATGG AAAAAATATT 360
TAAATTGAT CAGATGGGAA GATGGTTTGT TGCTGGAGGG GCTGCTGTTG GTCTTGGAGC 420
ATTGTGCTAC TATGGCTTGG GACTGTCTAA TGAGATTGGA GCTATTGAAA AGGCTGTAAT 480
TTGGCCTCAG TATGTCAAGG ATAGAATTCA TTCCACCTAT ATGTACTTAG CAGGGAGTAT 540
TGGTTTAAAC GCTTTGTCTG CCATAGCAAT CAGCAGAACG CCTGTTCTCA TGAACCTTCAT 600
GATGAGAGGC TCTTGGGTGA CAATTGGTGT GACCTTTGCA GCCATGGTTG GAGCTGGAAT 660
GCTGGTACGA TCAATACCAT ATGACCAGAG CCCAGGCCCA AAGCATCTTG CTTGGTTGCT 720
ACATTCTGGT GTGATGGGTG CAGTGGTGGC TCCTCTGACA ATATTAGGGG GTCCTCTTCT 780
CATCAGAGCT GCATGGTACA CAGCTGGCAT TGTGGGAGGC CTCTCCACTG TGGCCATGTG 840
TGCGCCCACT GAAAAGTTTC TGAACATGGG TGCACCCCTG GGAGTGGGCC TGGGTCTCGT 900
CTTTGTGTCC TCATTGGGAT CTATGTTTCT TCCACCTACC ACCGTGGCTG GTGCCACTCT 960
TTACTCAGTG GCAATGTACG GTGGATTAGT TCTTTTCAGC ATGTTCTCTC TGTATGATAC1020
CCAGAAAGTA ATCAAGCGTG CAGAAGTATC ACCAATGTAT GGAGTTCAAA AATATGATCC1080
CATTAACTCG ATGCTGAGTA TCTACATGGA TACATTAAAT ATATTTATGC GAGTTGCAAC1140
TATGCTGGCA ACTGGAGGCA ACAGAAAGAA ATGAAGTGAC TCAGCTTCTG GCTTCTCTGC1200
TACATCAAAT ATCTTGTTTA ATGGGGCAGA TATGCATTAA ATAGTTTGTA CAAGCAGCTT1260
TCGTTGAAGT TTAGAAGATA AGAAACATGT CATCATATTT AAATGTTCCG GTAATGTGAT1320
GCCTCAGGTC TGCCTTTTTT TCTGGAGAAT AAATGCAGTA ATCCTCTCCC AAATAAGCAC1380
ACACATTTTC AATTCTCATG TTTGAGTGAT TTTAAAATGT TTTGGTGAAT GTGAAACTA1440
AAGTTTGTGT CATGAGAATG TAAGTCTTTT TTCTACTTTA AAATTTAGTA GGTTCCTGA1500
GTAATAAAA TTTAGCAAAC CTGTGTTTGC ATATTTTTTT GGAGTGCAGA ATATTGTAAT1560
TAATGTCATA AGTGATTGG AGCTTTGGTA AAGGGACCAG AGAGAAGGAG TCACCTGCAG1620
TCTTTTGTTT TTTTAAATAC TTAGAACTTA GCACTTGTGT TATTGATTAG TGAGGAGCCA1680
GTAAGAAACA TCTGGGTATT TGGAAACAAG TGGTCATTGG TTACATTCAT CTGCTGAACT1740
TAACAAAACCT GGTTCATCC TGGAACAGGG CACAGGTGAA TGCATTCTCT CTGCGGTTGG1800
CTCCCCAGTG GCCCGCCTTC CCATATAGGA TGTGGG 1836

```

**(2) INFORMATION ON SEQ ID NO. 271:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1220 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing

**(iii) HYPOTHETICAL:** NO

**(iii) ANTI-SENSE:** NO

**(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

**(vii) OTHER ORIGIN:**

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:**

```

TGAAGTTCTA AGAGCTTTCC AAGTTTGGGA AGGTGTCCGG GTTTTCTGCG ATTACTTCTC 60
TGAGCATGAA CGGAAGTCAC CCTTTGTGCC TTATGCGGTG ATTTTAATGA TAGGTGTCAT 120
ATATAGGACG GAGTAACTCG TTTACATTCT GTTCTTCTCG ATGCACTCAC AAGCGGGTAA 180
CTAGGTGACA AGAAAACAAA GATCTTATTC AAAAGAGGTC TTACAGCAAC CCAACGTCTC 240
ATCTTCCCAT AGTAAAGATG ACGGCGCCTT GAGGTAAGCT ACAGGCAACA CCACTTCCGC 300
GTTTCTCTTG CGCCCTGGTC CAAGATGGCG GATGAAGCCA CGCGACGTGT TGTGTCTGAG 360
ATCCCGGTGC TGAAGACTAA CGCCGGACCC CGAGATCGTG AGTTGTGGGT GCAGCGACTG 420
AAGGAGGAAT ATCAGTCCCT TATCCGGTAT GTGGAGAACA ACAAGAATGC TGACAACGAT 480
TGGTTCCGAC TGGAGTCCAA CAAGGAAGGA ACTCGGTGGT TTGGAAAATG CTGGTATATC 540
CATGACCTCC TGAATATGA GTTTGACATC GAGTTTGACA TTCCTATCAC ATATCCTACT 600
ACTGCCCCAG AAATTGCAGT TCCTGAGCTG GATGGAAAGA CAGCAAAGAT GTACAGGGGT 660
GGCAAAATAT GCCTGACGGA TCATTTCAAA CCTTTGTGGG CCAGGAATGT GCCCAAATTT 720
GGACTAGCTC ATCTCATGGC TCTGGGGCTG GGTCCATGGC TGGCAGTGGA AATCCCTGAT 780
CTGATTGAGA AGGGCGTCAT CCAACACAAA GAGAAATGCA ACCAATGAAG AATCAAGCCA 840
CTGAGGCAGG GCAGAGGGAC CTTTGATAGG CTACGATACT ATTTTCCTGT GCATCACACT 900
TAACTCATCT AACTGCTTCC CCGGACACCC TCCACCTCTA GTTGTACTA AGTAGCTGCA 960
GTAGGCATTG CTGGGAAGA AACAAACACA CACCAAACAG TACTGCTACT TAGTTTCTAA1020
GGCTGCACAG GGAAGGGAAA GACTGGGCTT TGGACAATCT AGAGGTAATT TATATCCGCC1080
CCCAGGTGGA GCAACATGCG ATTCTGGAGG CACGGGGGTA ACTGAAAGTG AGTACATATA1140
GTCTTTCTGG TTTCTGGAGA TAACCCATCA ATAAAAGCTG CTTCTCTG TAAAAAAA1200
AAAAAAAAA AAAAAAAAAA

```

1220

## (2) INFORMATION ON SEQ ID NO. 272:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1303 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:**

```

CGCAGTGC GC AGGCGTGGGG CTCTCTCCTT GTCAGTCGGC GCCGCGTGCG GGCTGGTGGC 60
TCTGTGGCAG CGGCGGCGGC AGGACTCCGG CACTATGAGC GGCTTCAGCA CCGAGGAGCG 120
CGCCGCGCCC TTCTCCCTGG AGTACCGAGT CTTCCCTCAA AATGAGAAAG GACAATATAT 180
ATCTCCATTT CATGATATTC CAATTTATGC AGATAAGGAT GTGTTTCACA TGGTAGTTGA 240
AGTACCACGC TGGTCTAATG CAAAAATGGA GATTGCTACA AAGGACCCCT TAAACCCTAT 300
TAAACAAGAT GTGAAAAAAG GAAAACTTCG CTATGTTGCG AATTTGTTCC CGTATAAAGG 360
ATATATCTGG AACTATGGTG CCATCCCTCA GACTTGGGAA GACCCAGGGC ACAATGATAA 420
ACATACTGGC TGTGTGGTG ACAATGACCC AATTGATGTG TGTGAAATTG GAAGCAAGGT 480
ATGTGCAAGA GGTGAAATAA TTGGCGTGAA AGTTCTAGGC ATATTGGCTA TGATTGACGA 540
AGGGGAAACC GACTGGAAAG TCATTGCCAT TAATGTGGAT GATCCTGATG CAGCCAATTA 600
TAATGATATC AATGATGTCA AACGGCTGAA ACCTGGCTAC TTAGAAGCTA CTGTGGACTG 660
GTTTAGAAGG TATAAGGTTT CTGATGGAAA ACCAGAAAAT GAGTTTGCGT TTAATGCAGA 720
ATTTAAAGAT AAGGACTTTG CCATTGATAT TATTTAAAGC ACTCATGACC ATTGGAAAGC 780
ATTAGTGACT AAGAAAACGA ATGGAAAAGG AATCAGTTGC ATGAATACAA CTTTGTCTGA 840
GAGCCCTTTC AAGTGTGATC CTGATGCTGC CAGAGCCATT GTGGATGCTT TACCACCACC 900
CTGTGAATCT GCCTGCACAG TACCAACAGA CGTGATAAG TGGTTCCATC ACCAGAAAAA 960
CTAATGAGAT TTCTCTGGAA TACAAGCTGA TATTGCTACA TCGTGTTTCA CTGGATGTAT1020
TAGAAGTAAA AGTAGTAGCT TTTCAAAGCT TTAAATTTGT AGAACTCATC TAACTAAAGT1080
AAATTCTGCT GTGACTAATC CAATATACTC AGAATGTTAT CCATCTAAAG CATTTTTCAT1140
ATCTCAACTA AGATAACTTT TAGCACATGC TTAAATATCA AAGCAGTTGT CATTGGGAAG1200
TCACTTGTGA ATAGATGTGC AAGGGGAGCA CATATTGGAT GTATATGTTA CCATATGTTA1260
GGAAATAAAA TTATTTTGCT GAAACTTGGA AAAAAAAAAA AAA 1303

```

**(2) INFORMATION ON SEQ ID NO. 273:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 1586 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE:** partial cDNAs produced from individual ESTs by assembling and editing

**(iii) HYPOTHETICAL:** NO

**(iii) ANTI-SENSE:** NO

**(vi) ORIGIN:**

- (A) ORGANISM: HUMAN
- (C) ORGAN:

**(vii) OTHER ORIGIN:**

- (A) LIBRARY: cDNA library

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:**

```

CGGCTCGAGC GGCTCGAGAT TCGAGGTCGT GGTGGTCTTG GAAGAGCGTC GAGGGGGCCG 60
TGGACGTGGA ATGGGCCGAG GAGATGGATT TGATTCTCGT GGCAAACGTG AATTTGATAG 120
GCATAGTGGA AGTGATAGAT CTGGCCTGAA GCACGAGGAC AAACGTGGAG GTAGCGGATC 180
TCACAAGTGG GGAAGTGTCA AAGACGAATT AACAGAGTCC CCCAAATACA TTCAGAAACA 240
AATATCTTAT AATTACAGTG ACTTGATCA ATCAAATGTG ACTGAGGAAA CACCTGAAG 300
TGAAGAACAT CATCCAGTGG CAGACACTGA AAATAAGGAG AATGAAGTTG AAGAGGTAAA 360

```

```

AGAGGAGGGT CCAAAGAGA TGA CTTTGA TGAGTGAAG GCTATTCAA ATAAGGACCG 420
GGCAAAAGTA GAATTTAATA TCCGAAAACC AAATGAAGGT GCTGATGGGC AGTGAAGAA 480
GGGATTTGTT CTTCAATAA CAAAGAGTGA AGAGGCTCAT GCTGAAGATT CGGTTATGGA 540
CCATCATTTT CGGAAGCCAG CAAATGATAT AACGTCTCAG CTGGAGATCA ATTTTGGAGA 600
CCTTGCCCGC CCAGGACGTG GCGGCAGGGG AGGACGAGGT GGACGTGGGC GTGGTGGGCG 660
CCCAAACCGT GGCAGCAGGA CCGACAAGTC AAGTGCTTCT GCTCCTGATG TGGATGACCC 720
AGAGGCATTC CCAGCTCTGG CTTAAGTGA TGCCATAAGA CAACCTGGT TCCTTTGTGA 780
ACCCTTCTGT TCAAAGCTTT TGCATGCTTA AGGATTCCAA ACGACTAAGA AATTAAAAA 840
AAAAAGACTG TCATTCATAC CATTCACACC TAAAGACTGA ATTTTATCTG TTTTAAAAAT 900
GAACCTCTCC CGCTACACAG AAGTAACAAA TATGGTAGTC AGTTTGTAT TTAGAAATGT 960
ATTGGTAGCA GGGATGTTTT CATAATTTT AGAGATTATG CATTCTTCAT GAATACTTTT 1020
GTATTGCTGC TTGCAAATAT GCATTTCCAA ACTTGAATA TAGGTGTGAA CAGTGTGTAC 1080
CAGTTTAAAG CTTTCACTTC ATTTGTGTTT TTTAATTAAG GATTTAGAAG TTCCCCCAAT 1140
TACAACTGG TTTTAAATAT TGGACATACT GGTTTTAATA CCTGCTTTGC ATATTCACAC 1200
ATGGTCAACT GGGACATGTT AAAGTTTGA TGTCAAATT TTATGCTGTG TGAATACTA 1260
ACTATATGTA TTTTAACTTA GTTTTAATAT TTTCATTTT GGGGAAAAAT CTTTTTTCAC 1320
TTCTCATGAT AGCTGTTATA TATATATGCT AAATCTTTAT ATACAGAAAT ATCAGTACTT 1380
GAACAAATTC AAAGCACATT TGGTTTATTA ACCCGTGGCT GCCCTGGCAT GGGGCCCAT 1440
TGGGGTCCAA ATTATACTG ATTTACATTT TCAGCGATAT TACTTTTAAA TGCCTGAGTT 1500
CCCATTTAAA ATCTAACTAG ACACCTAATG GGAAGTGGT TAACCACTAT GTGGTAGCCA 1560
CGGGCCAG

```

## (2) INFORMATION ON SEQ ID NO. 274:

### (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 144 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: ORF

### (iii) HYPOTHETICAL: yes

### (vi) ORIGIN

- (A) ORGANISM: HUMAN

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

```

KQVKCAKVS YLLFLFYCAI DSCIKFVNAG SSWLSSVTLW SMSSVSLSAS NVGRVRIKSE 60
GCSTGDKLSL GVPASKATEP ISFRRRSSCS LCCWLSALAS DFFRRSYSGR YLSYSSAAL120
VTCTKSSNP VPRTAETPTT LSEL

```

## (2) INFORMATION ON SEQ ID NO. 275:

### (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: ORF

### (iii) HYPOTHETICAL: yes



- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 401 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

```
MPNFCAAPNC TRKSTQSDLA FFRFPRDPA CQKWVENCRR ADLEDKTPDQ LNKHYRLCAK 60
HFETSMICRT SPYRTVLRDN APTIFDLTS HLNPHSRHR KRIKELSEDE IRTLKQKKID120
ETSEQEQKHK ETNNSNAQNP SEEEGEGQDE DILPLTLEEK ENKEYLKSLE EILILMGKQN180
IPLDGHEADE IPEGLFTPDN FQALLECRIN SGEEVLRKRF ETTAVNTLFC SKTQQRQMLE240
ICESCIREET LREVRDSHFF SIITDDVVDI AGEHLPVLV RFVDESHNLR EEFIGFLPYE300
ADAEILAVKF HTMITKWL NMEYCRGQAY IVSSGFSSKM KVVASRLLEK YPQAIYTLCS360
SCALNMWLAK SVPVMGVSA LGTIEEVCSF FHXITTAER T 401
```

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```
MLISGTLSHG TTQIQYXXEE HHADMYRSDL PNPDTLSAEL HCWRIKWKHR GKDIPLPSTI 60
YEALHLPDIK FFPNVYALLK VLCILPVMKV ENERYENGTK ASLKHI 106
```

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 398 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF



(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

```
GRKCNKFWDN AQTSGIEEPS ETKGSMQKSK FKYKLVPEEE TTASENTEIT SERQKEGIKL 60
TIRISSRKKK PDSPPKVLEP ENKQEKTEKE EEKTNVGRIL RRSRPRISPT AKVAEIRDQK120
ADKKRGEDED EEEEESTALQ KTDKKEILKK SEKDTNSKVS KVKPKGKVRW TGSRTGRWK180
YSSNDESEGS GSEKSSAASE EEEEESEEA ILADDDPEPK KCGLPNHPEL ILLCDSCDSG240
YHTACLRPPL MIIPDGEWFC PPCQHKLCE KLEEQLQDLD VALKKKERA RRKERLVYVG300
ISINIIPPQ EPDFSEDQEE KKKDSKSKA NLLERRSTR RKCISYRFDE FDEAIDEAIE360
DDIKEADGGG VGRGKDISTI TGRGKDIST ILDEKIIT 398
```

(2) INFORMATION ON SEQ ID NO. 281:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 198 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

```
SSEKSGSCGG MMFSILIPTY TKRSFLRSAR SFFFKATSKS CNCSSNFSQS SLCWQGGQNH 60
SPSGMIIRGG RRQAVWYPLS QESHRISSG WFGPHFLHG SSSSARMAS LSFSSSSSEA120
ADDFSLPDPS LSSLLEYFHL PRVREPVHRT LPLGFTLLTL EFVSFSDFFK ISFLSVFCKA180
VDSSSTSSSP SPLFLSAF 198
```

(2) INFORMATION ON SEQ ID NO. 282:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 202 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:**

GRLPFSGRGR GKKVTSKGDGV ASLPLKLGRL FGGVTRGFNM RIEKCYFCSG PIYPGHGMMF 60  
 VRNDCKVFRF CKSKCHKNEK KKRNPVKVRW TKAFRKAAGK ELTVDNSFEF EKRRNEPIKY120  
 QRELWNKTID AMKRVEEIKQ KRQAKFIMNR LKKNKELQKV QDIKEVKQNI HIRAPLAGK180  
 GKQLEEKMVQ QLQEDVDMED AP 202

**(2) INFORMATION ON SEQ ID NO. 283:**

- (i) SEQUENCE CHARACTERISTIC:**  
 (A) LENGTH: 84 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: ORF**

**(iii) HYPOTHETICAL: yes**

**(vi) ORIGIN**  
 (A) ORGANISM: HUMAN

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:**

IIHCKLFTSC FPECFGPPNF ARIALLFKVF MTFREKSEH LAIVADEHHA VSRIDGPRTE60  
 ITLFDTHVEP ACNPTKQTPK LERK 84

**(2) INFORMATION ON SEQ ID NO. 284:**

- (i) SEQUENCE CHARACTERISTIC:**  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: ORF**

**(iii) HYPOTHETICAL: yes**

**(vi) ORIGIN**  
 (A) ORGANISM: HUMAN

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:**

RLEPRSVTRS RRAVSRLSAR PGKVSAMAF LASGPYLTHQ QKVLRLYKRA LRHLESWCVQ 60  
 RDKYRYFACL MRARFEEHKN EKDMAKATQL LKEABEEFWY RQHPQPYIFP DSPGGTSYER120  
 YDCYKVPEWC LDDWHPSEKA MYPDYFAKRE QWKKLRRESW EREVKQLQEE TPPGGPLTEA180  
 LPPARKEGDL PPLWWYIVTR PRERPM 206

**(2) INFORMATION ON SEQ ID NO. 285:**

- (i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 139 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

PLVPSFPSAV SSTVLSWQSN QDTLPSQKDA SHLSTILGPC SNRISHRRCP QESQGRCAV 60  
 DADGTRILPR PPSAAGWPSP YPFHSYVLQT GLSSNKQSIG ICLSGRTTTR GGVAPAYKAA120  
 TPFADGSGRV PTPRTPLRR 139

## (2) INFORMATION ON SEQ ID NO. 286:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

LMMTIYALSN EFAFKINEEQ LSFFPLLSVQ LWHAQRFLLD SWSGVIPFF FSCSCLPFLY60  
 PPRWRQIHDL KDTQYLLNSS 80

## (2) INFORMATION ON SEQ ID NO. 287:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 80 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

LMMTIYALSN EFAPKINEEQ LSFFPLLSVQ LWHAQRFLD SWSGVIPFF FSCSCLPFLY60  
 PPKWRQIHDL KDTQYLLNSS 80

## (2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 206 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSAF LLLVALSYTL ARDTTVKPGA 60  
 KKDTKDSRPK LPQTLRSGWG DQLIWTQTYE EALYKSKTSN KPLMIHHLD ECPHSQALKK120  
 VFAENKEIQK LAEQFVLLNL VYETTDKHLN PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180  
 YAYEPADTAL LLDNMKKALK LLKTEL 206

## (2) INFORMATION ON SEQ ID NO. 289:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 77 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60  
 LRHMKKLYIN PRQATNP 77

## (2) INFORMATION ON SEQ ID NO. 290:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 160 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

GGXGXQLLXP XAXQGXPAA S CXXQDVHLXR CXTVVRWYQR ITGMPXXAPT RNFSKFQRXV 60
MDLHGFPKEX GQXEXQEXLQ WEGRSSSGKC RISXSXLPXS TIXXFLKXXW XXIRXQSPXT120
WXRTYLRLGS ISEFSPGSCL PNWLEGKPRM TXAKWPKFFL                               160
  
```

## (2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 150 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

RHXPLXLGXH GHRAHSCLGW SQXALWDXAW GLXXXGSXQX RKKEAXWCVX VGXVGXCXXP 60
XEXMXXGFQEQ NXXGPNXXV SXLGXXXWNR XAEKNMXGCC AKXVNXXMDH XXGFQXRQIR120
GLCSHAHTGX NCHVSXSGSD TQLCXGLSFM                               150
  
```

## (2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 86 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

RAAKILKGGL QEVAEQLELE RIGPQHQAGS DSLLTGMAFF KMREMFEDH IDDAKYCGHL60  
YGLGSGSSYV QNGTGNAYEE EANKQS 86

(2) INFORMATION ON SEQ ID NO. 293:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 64 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

IKAKFNLNAF FFFFLLRSEI GTVILSTERQ TIKWAMKGGG KVLIVRGIQ PEIKPIYKXV60  
CSSK 64

(2) INFORMATION ON SEQ ID NO. 294:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 226 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ASTIMDLLFG RRKTPEELLR QNQRALNRAM RELDRERQKL ETQEKKIID IKKMAKQGQM 60  
DAVRIMAKDL VRTRYVRKF VLMRANIQAV SLKIQTLKSN NSMAQAMKGV TKAMGTMNRQ120  
LKLPQIQKIM MEFERQAEIM DMKEEMMND A IDDPMGDEED EEESDAVVSQ VLDELGLSLT180  
DELSNLPSTG GSLSVAAGGK KAEAAASALA DADADLEERL KNLRRD 226

## (2) INFORMATION ON SEQ ID NO. 295:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 166 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

KILGIHWLSR SGRGTQSLRR FLSRSSRSAS ASARAEAAAS AFFPPAATLS EPPVEGRFDS 60  
 SSVRLSPSSS RTWDTTASLS SSSSSSPMGS SMASFISSF ISMISACRSN SIMIFWIWGN120  
 FSCLFMVPMA LVTPFMACAI ELLDLSVWIL RDTAWMLARI NTNLR 166

## (2) INFORMATION ON SEQ ID NO. 296:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 233 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

## (vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

KPEGARRVQF VMGLFGKTQE KPPKELVNEW SLKIRKEMRV VDRQIRDIQR EEEKVKRSVK 60  
 DAAKKGQKDV CIVLAKEMIR SRKAVSKLYA SKAHMNSVLM GMKNQLAVLR VAGSLQKSTE120  
 VMKAMQSLVK IPEIQATMRE LSKEMMKAGI IEEMLEDTFE SMDDQEEMEE EAEMEIDRIL180  
 FEITAGALGK APSKVTDALP EPEPPGAMAA SEDEGEEMEEA LEAMQSRLAT LRS 233

## (2) INFORMATION ON SEQ ID NO. 297:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 129 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

LMPFQSQNLO ERWLPQMRG RKRRLWRPCS PGWPHSAARG CLPRWVCTHS SQELPFYVSL 60  
 ALHLCCEDYH FGEQSVCLFS FSAQVLGSQR DCSYKSGINK CIIFRSIDRY ILLWGGERNP120  
 SAHEALLKI 129

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 351 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TWCTTTMLAA RLVCLRTLPS RVFHPAFTKA SPVVKNSITK NOWLLTPSRE YATKTRIGIR 60  
 RGRTGQELKE AALEPSMEKI FKIDQMGRWF VAGGAAVGLG ALCYYGLGLS NEIGAIEKAV120  
 IWPQYVKDRI HSTYMYLAGS IGLTALSAIA ISRTPVLMNF MMRGSWVTIG VTFAAMVGAG180  
 MLVRSIPYDQ SPGPKHLAWL LHSGVMGAVV APLTILGGPL LIRAAWYTAG IVGGLSTVAM240  
 CAPSEKFLNM GAPLGVGLGL VEVSSLGSMF LPPTTVAGAT LYSVAMYGGL VLFSMFLLYD300  
 TQKVIKRAEV SPMYGVQKYD PINSMLSIYM DTLNIFMRVA TMLATGGNRK K 351

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 147 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN



## (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RVAPATVVGG RNIDPNEDTK TRPRTPRGA PMERNFSLGA HMATVERPPT MPAVYHAALM 60  
 RRGPPNIVRG ATTAPITPEC SNQARCFGPG LWSYGIDRTS IPAPTMAAKV TPIVTQEPLI120  
 MKFMRTGVLL IAMADKAVKP ILPAKYI 147

## (2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 188 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

RRLEVSyrQH HFRVSLAPWS KMADEATRRV VSEIPVLKTN AGPRDRELWV QRLKEEYQSL 60  
 IRYVENNKNA DNDWFRLESN KEGTRWFGKC WYIHDLLKYE FDIEFDIPIT YPTTAPEIAV120  
 PELDGKTAKM YRGGKICLTD HFKPLWARNV PKFGLAHLMA LGLGPWLAVE IPDLIQKGV180  
 QHKEKCNQ 188

## (2) INFORMATION ON SEQ ID NO. 301:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 172 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

SKFGHIPGPQ RFEMIRQAYF ATPVHLCCLS IQLRNCNFWG SSRICDRNVK LDVKLIFQEV 60  
 MDIPAFSKPP SSFLVGLQSE PIVVSILVVL HIPDKGLIFL LQSLHPQLTI SGSGVSLQHR120  
 DLRHNTSRGF IRHLGPGRKR NAEVLPVAY LKAPSSLLWE DETLGCKTS FE 172

## (2) INFORMATION ON SEQ ID NO. 302:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 320 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AVRRRGALSL SVGAACGLVA LWQRRRQDSG TMSGFSTEER AAPFSLEYRV FLKNEKGQYI 60  
 SPFHDIPIYA DKDVFHVMVE VPRWSNAKME IATKDPLNPI KQDVKKGKLR YVANLFPYKG120  
 YIWNYGAIPQ TWEDPGHNDK HTGCCGDNDP IDVCEIGSKV CARGEIIGVK VLGILAMIDE180  
 GETDWKVI AI NVDDPDAANY NDINDVKRLK PGYLEATVDW FRRYKVPDGK PENEFAFNAE240  
 FKDKDFAIDI IKSTHDHWKA LVTKKTNGKG ISCMNTTLE SPFKCDPDAA RAIVDALPPP300  
 CESACTVPTD VDKWFHHQKN 320

## (2) INFORMATION ON SEQ ID NO. 303:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: ORF

## (iii) HYPOTHETICAL: yes

## (vi) ORIGIN

- (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

RVLCSNLHFC IRPAWYFNYH VKHILICINW NIMKWRYILS FLIFEEDSVL QGEGRGALLG60  
 AEAHHSAGVL PPPLPQSHQP ARGAD 85

## (2) INFORMATION ON SEQ ID NO. 304:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGGSGS 60  
 HNWGTVKDEL TESPKEYIQKQ ISYNYSDLDQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120  
 EEGPKEMTLD EWKAIONKDR AKVEFNIRKP NEGADGQWKK GFVLHKSSE EAAEDSVMD180  
 HHFRKPANDI TSQLEINFGD LGRPGRGGRG GRGGRGRGGR PNRGSRTDKS SASAPDVDDP240  
 EAFPALA 247

(2) INFORMATION ON SEQ ID NO. 305:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 78 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

SFGILKHAKA LNRRVHKGTR VVLWHPVKPE LGMPLGHPHQ EQKHLTCRSC CHGLGAHHAH60  
 VHLVLPGRHV LGGQGLQN 78

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 293 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:**

```

ATRGAEQDGG ASAARPRRW AGLLQRAAP CSLLPRLRTW TSSSNRSRED SWLKSLFVRK 60
VDPRKDAHSN LLAKKETSNI YKLQFHNVPK ECLEAYNKIC QEVLPKIHED KHYPCTLVGT120
WNTWYGEQDQ AVHLWRYEGG YPALTEVMNK LRENKEFLEF RKARSDMLLS RKNQLLLEFS180
FWNEPVPRSG PNIYELRSYQ LRPGMTIEWG NYWARAIRFR QDGNEAVGGF FSQIGQLYMV240
HHLWAYRDLQ TREDIRNAAW HKHGWEELVY YTVPLIQEME SRIMIPLKTS PLQ          293

```

**(2) INFORMATION ON SEQ ID NO. 307:****(i) SEQUENCE CHARACTERISTIC:**

- (A) LENGTH: 208 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

**(ii) MOLECULE TYPE: ORF****(iii) HYPOTHETICAL: yes****(vi) ORIGIN**

- (A) ORGANISM: HUMAN

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:**

```

AHRNSTALLE GRGLQWDHDS GFHFLNKWNC VIYQFLPAMF VPCCIPYVFP GLKIPVSPKM 60
VHHVQLPNLR EESSDGFVTI LSEADCTSPV IAPFNHGSWS ELVRPEFIYI RSGSWHRLIP120
ETELQQELIL PGEKHVTSCL TKFQKFLIFS EFIHDFCEGW IASFIPPEVD SLVLLAIPRV180
PSPHQSTRVV FIFVNLWQHL LTNEVVCF          208

```

WO 99/53040

PCT/DE99/01087

**Claims**

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

- a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57 and 258-273
- b) an allelic variation of the nucleic acid sequences named under a)

or

- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, 258-273, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID Nos. 1-123 and 258-273, characterized in that it is expressed elevated in ovarian tumor tissue.

4. Nucleic acid sequence Seq. ID Nos. 27, 32, 42, 46, 67, 76, 78, 80, 85, 88, 90, 108 and 112, wherein they are also expressed elevated in breast tumor tissue.

5. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-10, 12, 13, 15, 16, 18-36, 38-57, and 258-273 for use as vehicles for gene transfer.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

7. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

8. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 7.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

10. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

11. A nucleic acid sequence according to one of claims 1 to 10, which codes at least one partial sequence of a bioactive polypeptide.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 10, together with at least one control or regulatory sequence.

13. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

14. An expression cassette according to one of claims 12 and 13, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

15. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

16. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 15.

17. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

18. Host cell according to claim 17, wherein it is a prokaryotic or eukaryotic cell system.

19. Host cell according to one of claims 17 or 18, wherein the prokaryotic cell system is *E. coli* and the eukaryotic cell system is an animal, human or yeast cell system.

20. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 17 to 19 are cultivated.

21. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 124-257 and 274-307, which can be obtained according to claim 20.

22. An antibody according to claim 20, wherein it is monoclonal.

23. An antibody according to claim 20, wherein it is a phage display antibody.

24. Polypeptide partial sequences according to sequences Seq. ID Nos. 124-257 and 274-307.

25. Polypeptide partial sequences according to claim 24, with at least 80% homology to these sequences.

26. Polypeptide partial sequences according to claim 22, with at least 90% homology to these sequences.

27. A polypeptide that is developed from a phage display and that can bind to the polypeptide partial sequences according to claim 24.

28. Use of polypeptide partial sequences according to claim 24 in a phage display process.

29. Use of nucleic acid sequences according to claim 3 in a phage display process.

30. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 124-257 and 274-307 as tools for finding active ingredients against ovarian cancer.

31. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-123 and 258-273 for expression of polypeptides that can be used as tools for finding active ingredients against ovarian cancer.

32. Use of nucleic acid sequences Seq. ID Nos. 1-123 and 258-273 in sense or antisense form.

33. Use of polypeptide partial sequences Seq. ID Nos. 124-257 and 274-307 as pharmaceutical agents in gene therapy for treatment of ovarian cancer.

34. Use of polypeptide partial sequences Seq. ID Nos. 124-257 and 274-307 for the production of a pharmaceutical agent for treatment of ovarian cancer.

35. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 124-257 and 274-307.

36. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.



37. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

38. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-123 and 258-273.

39. Use of the genomic genes according to claim 36, together with suitable regulatory elements.

40. Use according to claim 39, wherein the regulatory element is a suitable promoter and/or enhancer.

41. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

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## Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
~50,000 individual ESTs

Tumor tissue  
~50,000 individual ESTs

## Priority list

High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

Low

~8,000 contigs  
+  
~25,000 individual  
sequences

~8,000 contigs  
+  
~25,000 individual  
sequences

## Comparison of databases

normal tissue-  
specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)



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## Principle of EST Assembly

~50,000 ESTs per tissue

Assembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Individual sequences

Contigs increasing in  
number and lengthIterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000-6000 contigs

~25,000 other individual  
sequences~30,000 consensus-  
sequences per tissue

Figure 2a

REPLACEMENT PAGE (RULE 26)

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# Prinzip der EST-Assemblierung

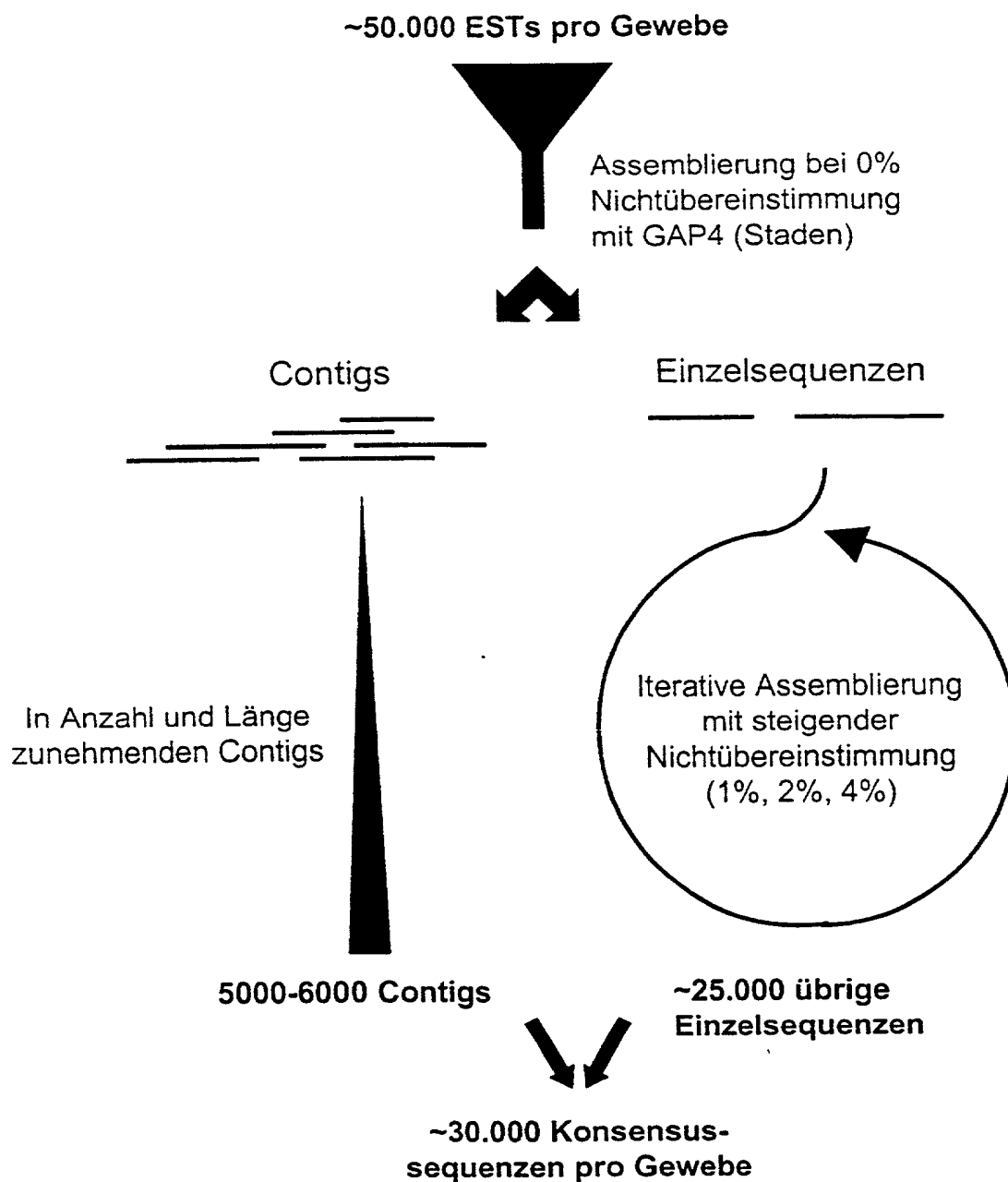


Fig. 2a

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~50,000 ESTs of a tissue (e.g.: uterus tumor)

GAP4 Assembly 1st Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 0

GAP4 Database 1  
Contigs 1  
Individual sequences 1

unassembled  
ESTs

GAP4 Assembly 2nd Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 1

GAP4 Database 2  
Contigs 2  
Individual sequences 2

unassembled  
ESTs

GAP4 Assembly 3rd Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 2

GAP4 Database 3:  
Contigs 3  
Individual sequences 3

unassembled  
ESTs

Figure 2b1

REPLACEMENT PAGE (RULE 26)

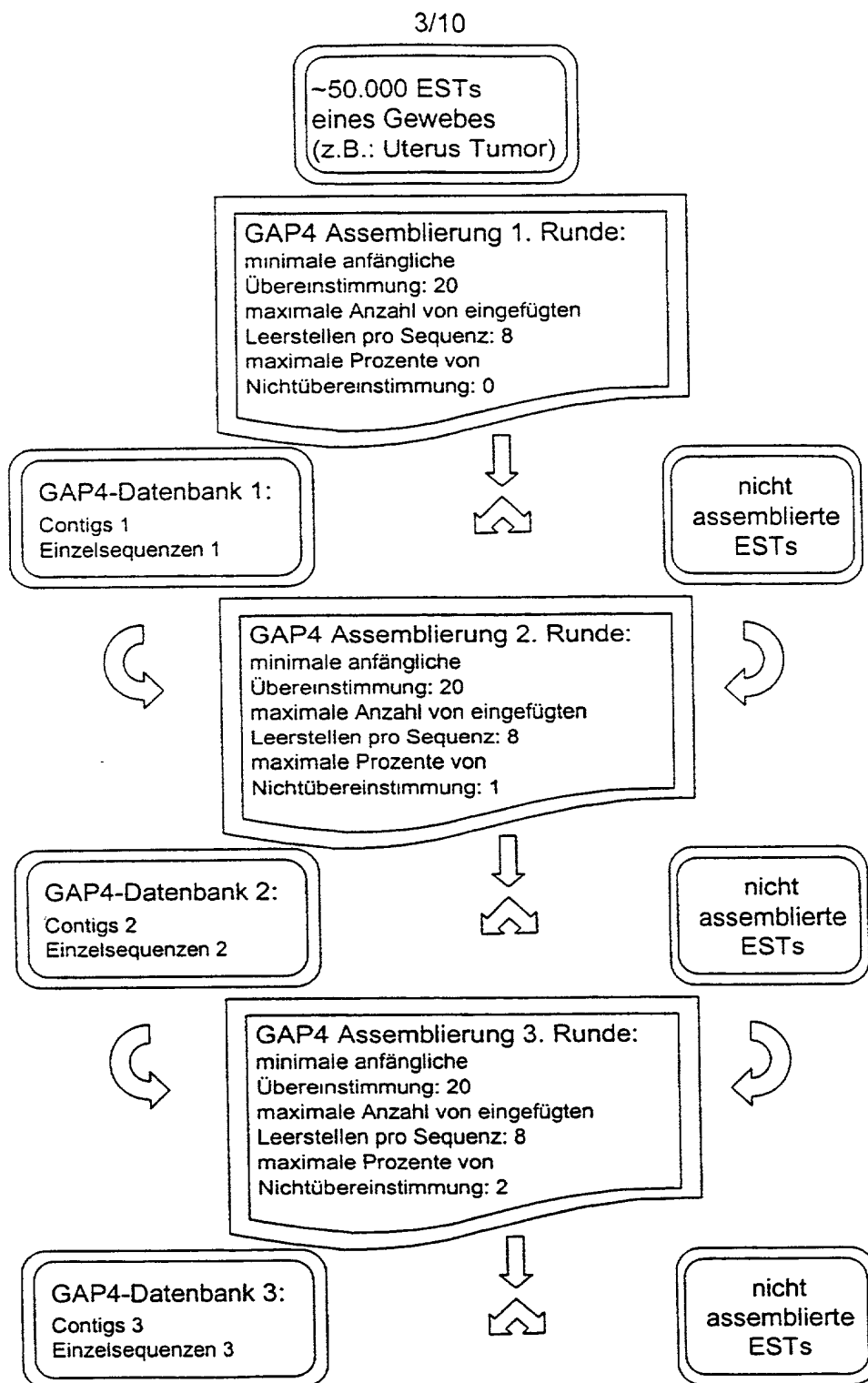


Fig. 2b1

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GAP4 Database 3:  
Contigs 3  
Individual sequences 3

unassembled  
ESTs

Consensus 3

GAP4 Assembly 4th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 2

GAP4 Database 4:  
Contigs 4  
Individual sequences 4

unassembled  
ESTs

Consensus 4

GAP4 Assembly 5th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 4

GAP4 Database 5:  
Contigs 5  
Individual sequences 5

unassembled  
ESTs 5

Consensus 5

Individual sequences 5

Figure 2b2

REPLACEMENT PAGE (RULE 26)



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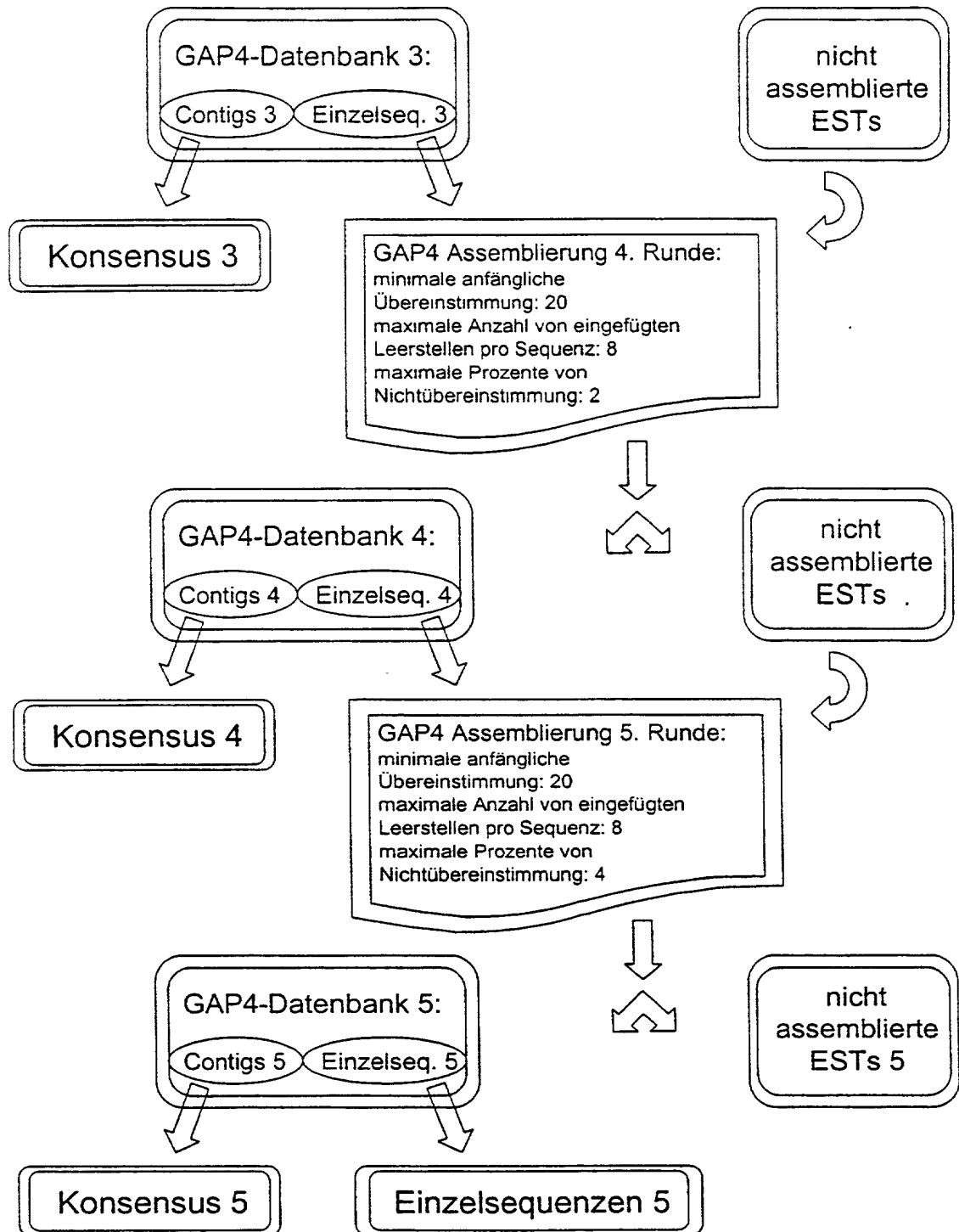


Fig. 2b2

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Consensus 3

Individual sequences 5

Consensus 4

unassembled  
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:  
minimum initial match: 20  
maximum number of inserted  
empty spaces per sequence: 8  
maximum percent mismatch: 4

Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Figure 2b3

REPLACEMENT PAGE (RULE 26)

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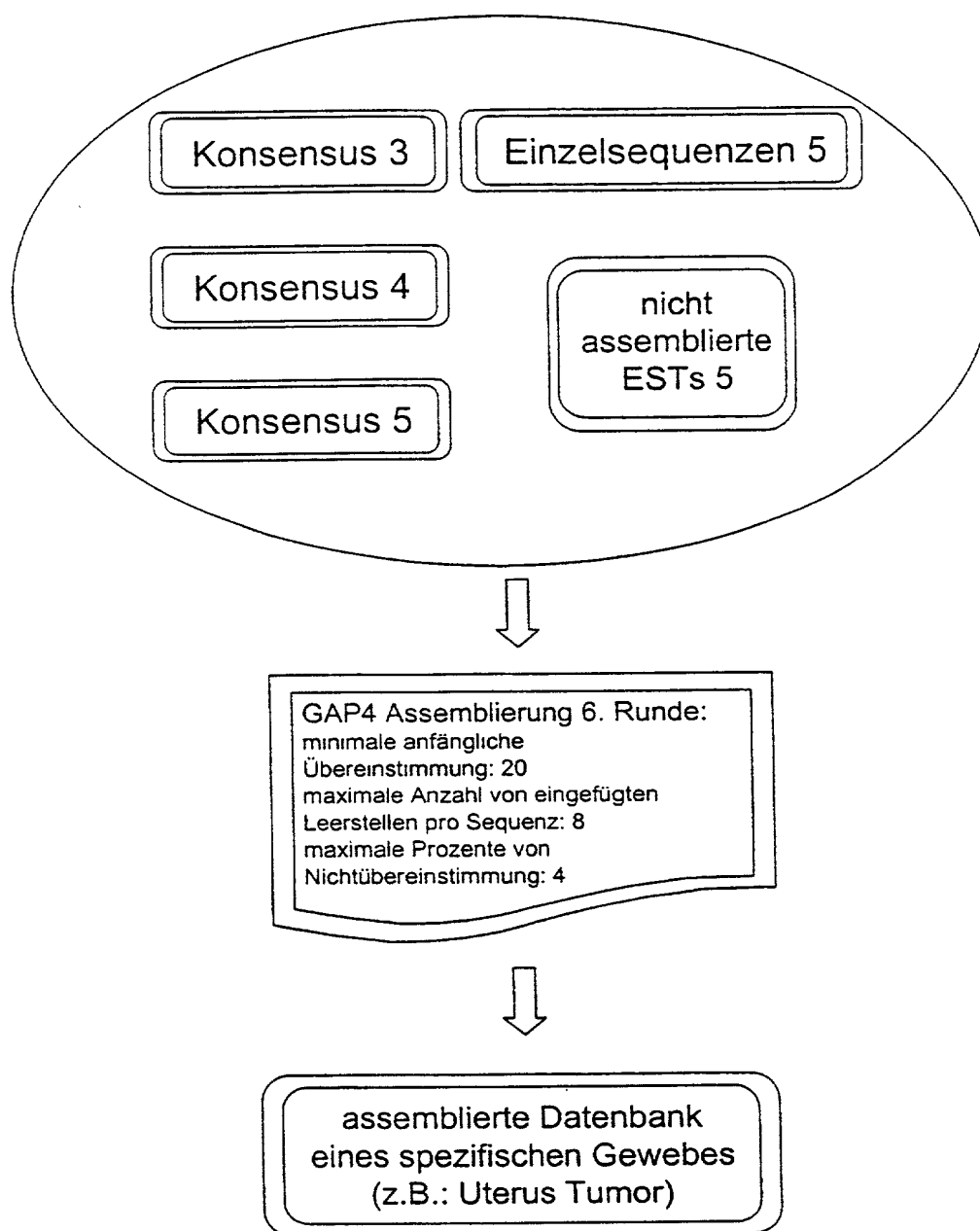


Fig. 2b3

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6/10

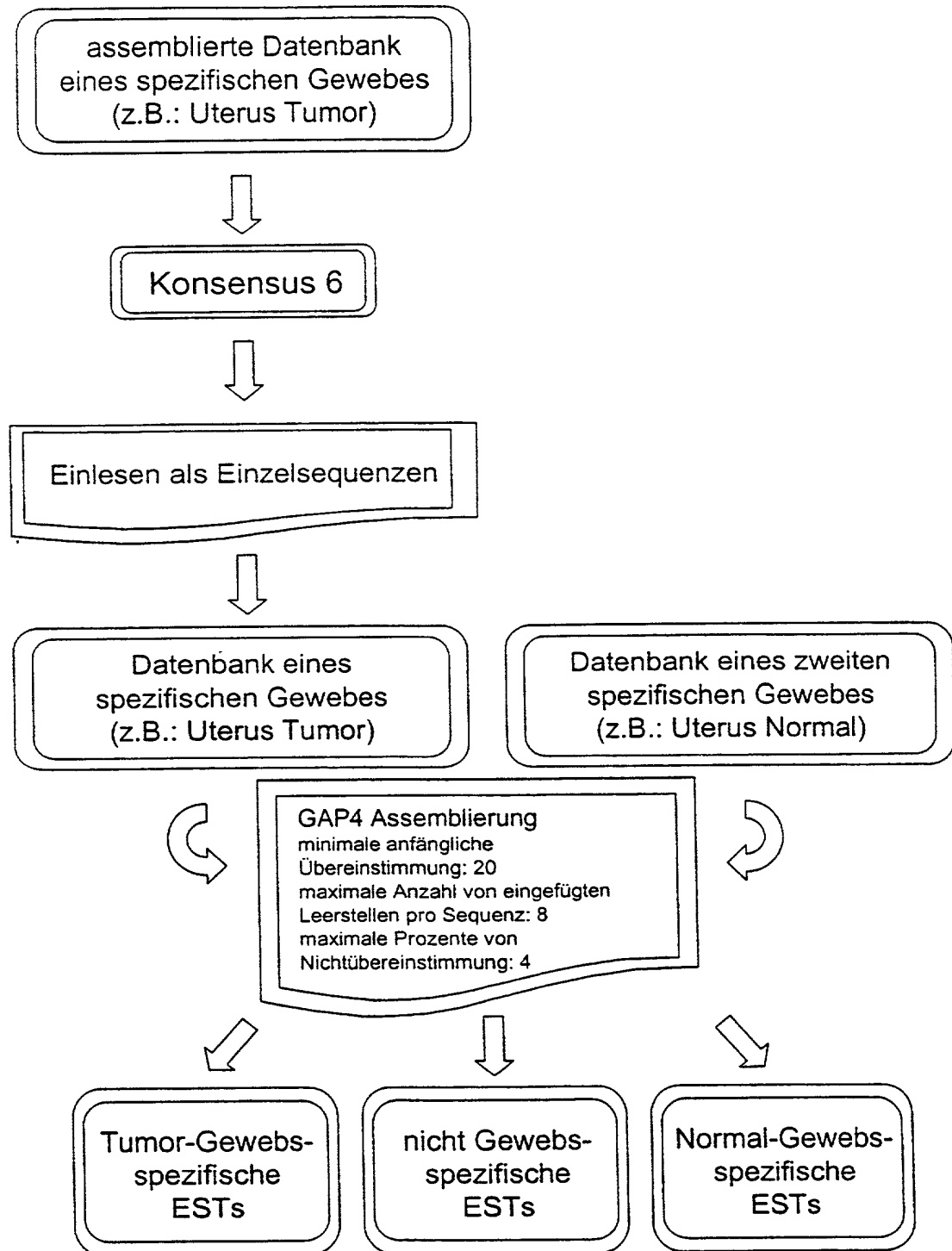


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

Assembly at 4% mismatch

Normal tissue  
Specific genes

Cancer tissue  
Specific genes

Genes expressed in both tissues

Figure 3

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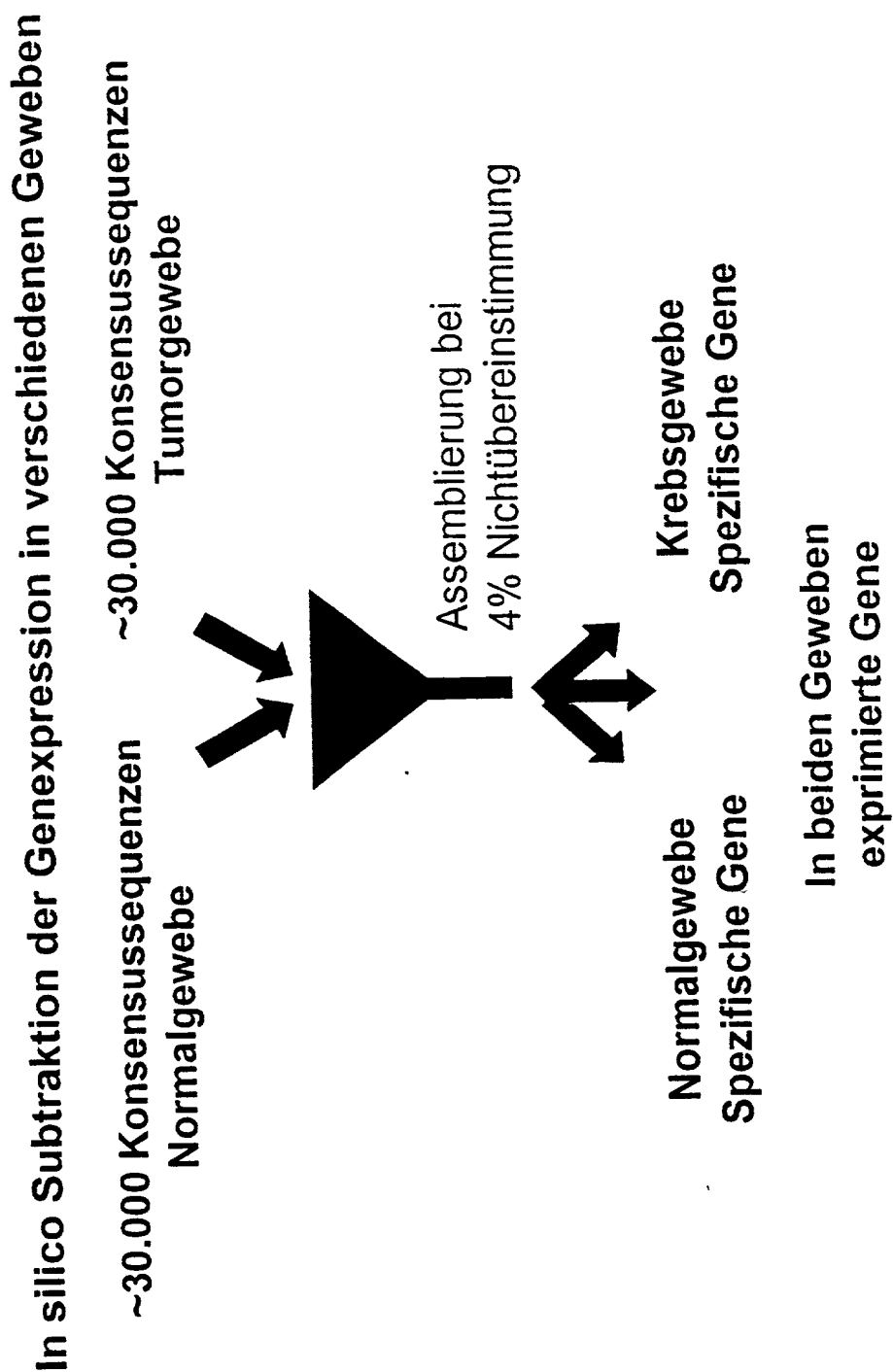


Fig. 3

Genes of interest

Determination of tissue-specific expression  
via electronic Northern (INCYTE LifeSeq and  
public EST databases)

Candidate genes for tumor suppressors or  
tumor activators

Figure 4a

REPLACEMENT PAGE (RULE 26)



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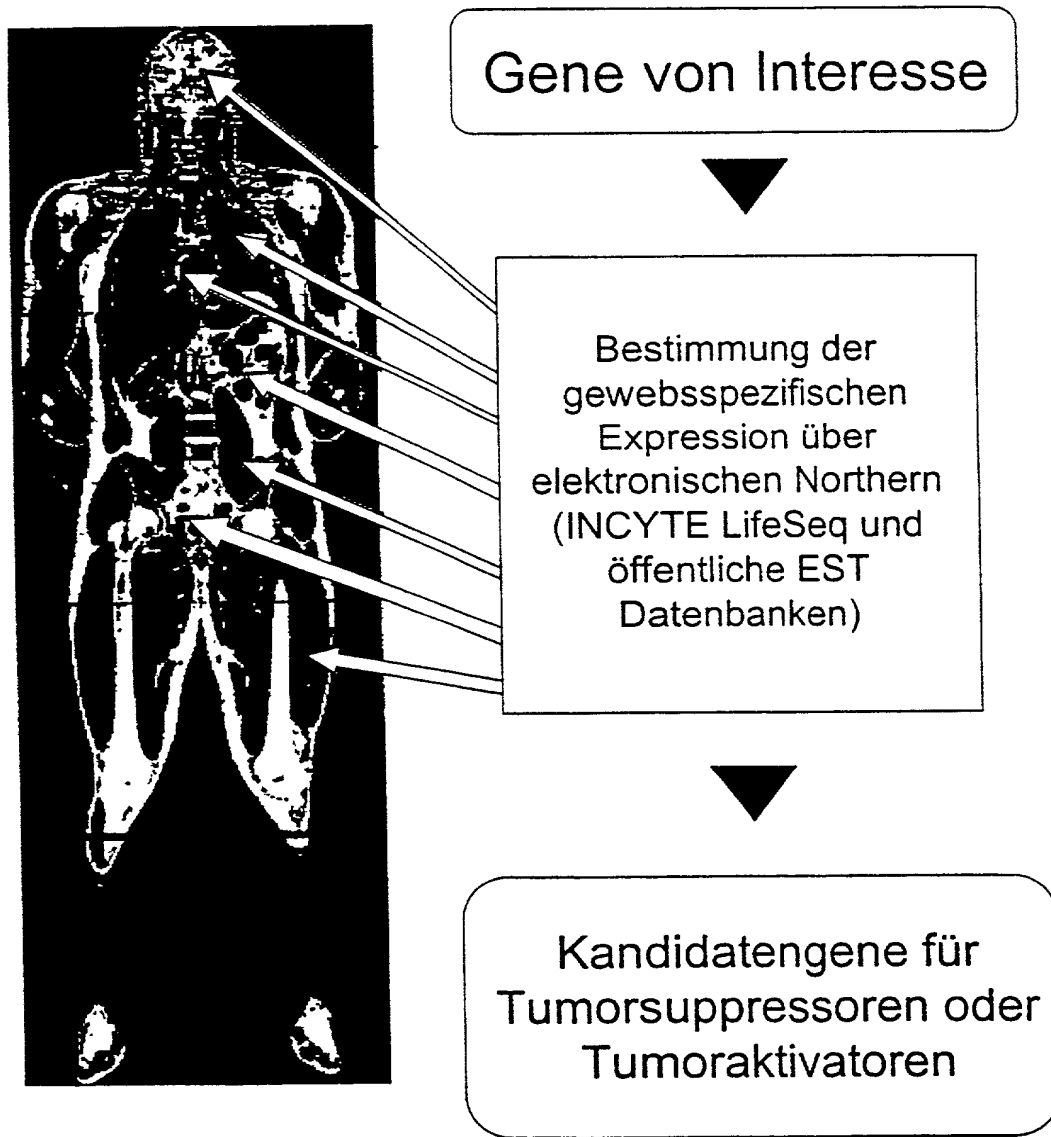


Fig. 4a

9/10

Partial cDNA sequence  
e.g., EST or contig  
S

...GCCTCAAGTTATC...

WHILE  $C_i > C_{i-1}$

Electronic Northern Blot

Fisher's Exact Test IF  $H_0$  EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)



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Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon      Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

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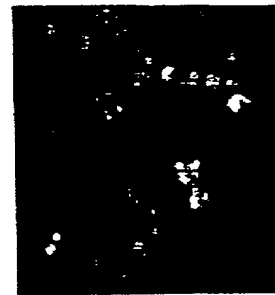
Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5

**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

**HUMAN NUCLEIC ACID SEQUENCES FROM OVARIAN TUMOR TISSUE**

the specification of which

☐ is attached hereto

☒ was filed on 7 APRIL 1999 as United States Application Number or PCT International Application Number PCT/DE99/01087 and (if applicable) was amended on \_\_\_\_\_

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims as amended by any amendment referred to above

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed

<b>PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119</b>			
APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 557.4	GERMANY	09/04/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

<b>PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)</b>	
APPLICATION NUMBER	FILING DATE

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

<b>PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120</b>		
APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544), John L. White (17,746); Anthony J. Zelano (27,969), Alan E. J. Branigan (20,565), John R. Moses (24,983), Harry B. Shubin (32,004); Brian P. Heaney (32,542), Richard J. Traverso (30,595), John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460), Catherine M. Joyce (40,668), Nancy J. Axelrod (44,014), James T. Moore (35,619), James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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 FAX (703) 243-6410

Attorney Docket Number SCH 1768**DECLARATION FOR PATENT APPLICATION**

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled.

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the specification of which

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☒ was filed on 7 APRIL 1999 as United States Application Number or PCT International Application Number PCT/DE99/01087 and (if applicable) was amended on \_\_\_\_\_

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**PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119**

APPLICATION NO.	COUNTRY	DAY/MONTH/YEAR FILED	PRIORITY CLAIMED
198 17 557.4	GERMANY	09/04/98	YES

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

**PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)**

APPLICATION NUMBER	FILING DATE

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I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

**PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120**

APPLICATION NO.	FILING DATE	STATUS — PATENTED, PENDING, ABANDONED

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: I. William Millen (19,544), John L. White (17,746); Anthony J. Zelano (27,969), Alan E. J. Branigan (20,565), John R. Moses (24,983), Harry B. Shubin (32,004); Brion P. Heaney (32,542), Richard J. Traverso (30,595), John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460), Catherine M. Joyce (40,668), Nancy J. Axelrod (44,014), James T. Moore (35,619), James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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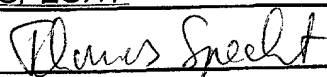
## Declaration for Patent Application (Continued)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

Full Name of sole or first inventor (given name, family name)

1-00 Thomas SPECHT

Signature



Date

29/08/00

Residence

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Citizenship

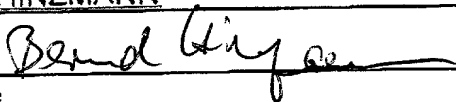
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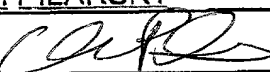
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4-00 Christian PILARSKY

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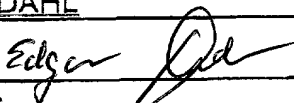
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6-00 Andre ROSENTHAL

Signature



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31/08/2000

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Citizenship

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Post Office Address Koppenplatz 10, D-10115 Berlin, Germany

☐ Additional joint inventors are named on separately numbered sheets attached hereto.

K:\PAT\Sch\1762\Decl wpd



I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon

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Bernd HINZMANN	
Signature <i>Bernd Hinzmann</i>	Date 25/08/00
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Armin SCHMITT	
Signature <i>Armin Schmitt</i>	Date September 4, 2000
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Andre ROSENTHAL	
Signature <i>Andre Rosenthal</i>	Date 31/08/2000
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Post Office Address Koppenplatz 10, D-10115 Berlin, Germany	

☐ Additional joint inventors are named on separately numbered sheets attached hereto.

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## Sequence Protocol

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422 Rec'd PCT/PTO 22 SEP 2000

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<210> 5
<211> 579
<212> DNA
<213> Homo sapiens

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<400> 5

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<210> 6
<211> 2809
<212> DNA
<213> Homo sapiens

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<400> 6

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<210> 7

<211> 910

<212> DNA

<213> Homo sapiens

<400> 7

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910

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<210> 8
<211> 1447
<212> DNA
<213> Homo sapiens

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1447

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<210> 9
<211> 671
<212> DNA
<213> Homo sapiens

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<400> 9
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671

```

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<210> 10
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<211> 803  
 <212> DNA  
 <213> Homo sapiens

<400> 10

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803

<210> 11

<400> 11

000

<210> 12

<211> 828

<212> DNA

<213> Homo sapiens

<400> 12

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828

<210> 13

<211> 552

<212> DNA

<213> Homo sapiens

<400> 13

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cttgtctaatt tc

552

&lt;210&gt; 14

&lt;400&gt; 14

000

&lt;210&gt; 15

&lt;211&gt; 993

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

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993

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&lt;210&gt; 16

&lt;211&gt; 2273

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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<210> 17

<400> 17

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<210> 18

<211> 986

<212> DNA

<213> Homo sapiens

<400> 18

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<210> 19

<211> 526

<212> DNA

<213> Homo sapiens

<400> 19

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gcacagaaca aattatttgg tcacagttac ttttaactct ttcagcaatg cctgagtcct180
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tcattccaatg gattaaaacc ctctcttttg gtggcagtg aacgggtatga tacctaaaaa420
gaaaaaagag ttaatcacct ctctgggata tgaatgctat tagaagtttg ttgacttctc480
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<210> 20

<211> 1765

<212> DNA

<213> Homo sapiens

<400> 20

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gcacacacat taagaaagca cacacactag gcttctagtt gggctaatta aaatctctat 180
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<210> 21

<211> 746

<212> DNA

<213> Homo sapiens

<400> 21

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tctcaaagggt gtccacaaag caaaaaaatc agaccaaatg ctaagagcaa gtaacttata660
cttcaccacc tggacatggc actggcaaaa gtcacttcag cattagaaca gtaatgtttt720
tgctaaatta ctaaaataat agccgc 746

```

<210> 22

<211> 659

<212> DNA

<213> Homo sapiens

<400> 22

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agcagactca caccagaact acattccctg gccccctgcc tgtgtgcttc tggccaggcc 60
ttggttggca agtctgaccc gagaaaagga tctgcagaaa atcagactat gggatcactt120
tggttgtgca ttgggaatga cattctttcc caccacagga aaacctttgg gactttcaga180
gacattgtgg ctagccaacc acatgggtcag cctcaaagtt gagaggctca gtaaccctcc240
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atatccaaga gaagatgaaa ctaaatggag aaattgaaat acatctactg gaagaaaaga540
tccaattcct gaaaatgaag attgctgaga agcaaagaca aatttgtgtg acccagaaat600
tactgccagc caagagggtcc ctggatgccg acctagctgt gctccaaatt cagttttca 659

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<210> 23  
 <211> 357  
 <212> DNA  
 <213> Homo sapiens

<400> 23

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cgcatgtcgc agccgtgggg ctctctcctt gtcagtgcgc gccgcgtgcg ggctgggtggc 60
tctgtggcag cggcggcgcc aggactccgg cactatgagc ggcttcagca ccgaggagcg120
cgccgcgccc ttctccctgg agtaccgagt ctctctcaaa aatgagaaaag gacaatatat180
atctccattt catgatattc caatttatgc agataaggta aggcattcctt gtttttggac240
acagtctctt tactcagatc agctagttct acatatgaat tttcttatat gtctctcaac300
aagtgcctaa aatgcctcgt tgtgctgtga gtaaaggctt gttgattagg ctggggcg 357

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<210> 24  
 <211> 890  
 <212> DNA  
 <213> Homo sapiens

<400> 24

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cggaggcagc ggaaagccga gccaggcgcc tgcgcgtcgg gaagagtagg ttcagagtgc 60
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```

<210> 25  
 <211> 651  
 <212> DNA  
 <213> Homo sapiens

<400> 25

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cacctcgagt cgtgggtgcg ccagagagac aaataccgat actttgcttg ttgatgaga120
gcccggtttg aagaacataa gaatgaaaag gatatggcga aggccaccca gctgctgaag180
gaggccgagg aagaattctg gtaccgtcag catccacagc catacatctt ccctgactct240
cctgggggca cctcctatga gagatacgat tgctacaagg tcccagaatg gtgcttagat300
gactggcatc cttctgagaa ggcaatgtat cctgattact ttgccaaagag agaacagtgg360
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```

```

cctgggtgggc ctttaactga agctttgccc cctgcccga aggaaggtga tttgccccca480
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atctttcatg cttgcaagt aaatatgtta cagaacatgc acttgcccta ataaaaaatc600
agtgaatgg taaaaaaaaa agtgccattg tagtatgcaa taataagcgg c 651

```

```

<210> 26
<211> 1256
<212> DNA
<213> Homo sapiens

```

```
<400> 26
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ctcgagccga attcggctcg agctttcatc tgaccatcca tatccaatgt tctcatttaa 60
acattaccca gcatcattgt ttataatcag aaactctggt ccttctgtct ggtggcactt 120
agagtctttt gtgccataat gcagcagtat ggaggaggga ttttatggag aaatggggat 180
agtcttcatg accacaaata aataaaggaa aactaagctg cattgtgggt tttgaaaagg 240
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gaaaagggtta ttatacttct taacaattct ttttttcagg gacttttcta gctgtatgac 600
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aattccagct gatgggagac caaagaattt gcaagtggat ggtttgggtat cactgtaaat1200
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```

```

<210> 27
<211> 694
<212> DNA
<213> Homo sapiens

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```
<400> 27
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gacttcatta aacttatgac cgaaaaaaaa aaaa 694

```

```

<210> 28
<211> 1927
<212> DNA
<213> Homo sapiens

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<400> 28
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gcgagtattt attttttttt tttttttttt acagaaattg acctttattt gttgtactaa 60
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```

tcagtacctg tctgtgcaca ctgtaccatc tcagtccac tctgcctgta acttagaaaa 180
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ctttctactg tgtggctgtc tgctttgtgc tccttggcac tctgctccat cccacctga1920
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1927

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<210> 29

<211> 672

<212> DNA

<213> Homo sapiens

<400> 29

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672

```

<210> 30

<211> 269

<212> DNA

<213> Homo sapiens

<400> 30

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ccgcctccta gccgccgact cacacaaggc aggtgggtga ggaaatccag agttgccatg 60
gagaaaattc cagtgtcagc attcttgccg cttgtggcgc tctcctacaa tctggccagg120
gatagcacag tcaaacctgg agccaaaaag gacaggaagg agtctcgagc caaactgcgc180
cagacctctc ccagaagttg ggtgaacaa ctcactctgga ctcagacgta tgaagaagct240

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ctatataaat cgagactagc aactaaccc

269

<210> 31  
 <211> 604  
 <212> DNA  
 <213> Homo sapiens

<400> 31

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tgcgagggcg ggatagctgt ccaaggtctc cccagcact gaggagctcg cctgctgccc 60
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604

<210> 32  
 <211> 781  
 <212> DNA  
 <213> Homo sapiens

<400> 32

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781

<210> 33  
 <211> 304  
 <212> DNA  
 <213> Homo sapiens

<400> 33

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aactgaagaa gacagagacg caagagaaaa atccactgcc ttccaaagaa acgattgaac180
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304

<210> 34  
 <211> 1528  
 <212> DNA  
 <213> Homo sapiens

<400> 34

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&lt;210&gt; 35

&lt;211&gt; 499

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 35

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&lt;210&gt; 36

&lt;211&gt; 1396

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

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<210> 37

<400> 37

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<210> 38

<211> 808

<212> DNA

<213> Homo sapiens

<400> 38

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<210> 39

<211> 1139

<212> DNA

<213> Homo sapiens

<400> 39

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<210> 40

<211> 2177

<212> DNA

<213> Homo sapiens

<400> 40

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<210> 41

<211> 402

<212> DNA

<213> Homo sapiens

<400> 41

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<210> 42  
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 <212> DNA  
 <213> Homo sapiens

<400> 42

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1349
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<210> 43  
 <211> 3552  
 <212> DNA  
 <213> Homo sapiens

<400> 43

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&lt;210&gt; 44

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

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601

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&lt;210&gt; 45

&lt;211&gt; 2147

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 45

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&lt;210&gt; 46

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

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623

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&lt;210&gt; 47

&lt;211&gt; 781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 47

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<210> 48
<211> 1714
<212> DNA
<213> Homo sapiens

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<400> 48
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<210> 49
<211> 831
<212> DNA
<213> Homo sapiens

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<400> 49
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&lt;210&gt; 50

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

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&lt;210&gt; 51

&lt;211&gt; 2017

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

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2017

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<210> 52  
 <211> 856  
 <212> DNA  
 <213> Homo sapiens

<400> 52

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<210> 53  
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 <212> DNA  
 <213> Homo sapiens

<400> 53

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<210> 54  
 <211> 1912  
 <212> DNA  
 <213> Homo sapiens

<400> 54

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<210> 55

<211> 1962

<212> DNA

<213> Homo sapiens

<400> 55

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1962

```

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<210> 56
<211> 1458
<212> DNA
<213> Homo sapiens

<400> 56

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<210> 57
<211> 2188
<212> DNA
<213> Homo sapiens

<400> 57

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2188

&lt;210&gt; 58

&lt;211&gt; 1548

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 58

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&lt;210&gt; 59

&lt;211&gt; 1254

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

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<400> 60

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<212> DNA

<213> Homo sapiens

<400> 63

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<400> 64

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<210> 65

<211> 2213

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&lt;213&gt; Homo sapiens

&lt;400&gt; 65

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&lt;210&gt; 66

&lt;400&gt; 66

000

&lt;210&gt; 67

&lt;211&gt; 2878

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

```

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<210> 68

<211> 701

<212> DNA

<213> Homo sapiens

<400> 68

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701

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<210> 69

<211> 817

<212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

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&lt;210&gt; 70

&lt;211&gt; 2686

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

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&lt;210&gt; 71

&lt;400&gt; 71

000

&lt;210&gt; 72

&lt;211&gt; 922

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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&lt;210&gt; 73

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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&lt;210&gt; 74

&lt;211&gt; 1418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 74

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&lt;210&gt; 75

&lt;400&gt; 75

000

&lt;210&gt; 76

&lt;211&gt; 1712

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 76

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<210> 77

<400> 77

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<210> 78

<211> 1273

<212> DNA

<213> Homo sapiens

<400> 78

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<211> 2342

<212> DNA

<213> Homo sapiens

<400> 79

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&lt;210&gt; 84

<211> 3462  
 <212> DNA  
 <213> Homo sapiens

<400> 84

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3462

<210> 85

<211> 668

<212> DNA

<213> Homo sapiens

<400> 85

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gaaaaaaa
668

```

<210> 86

<211> 671

<212> DNA

<213> Homo sapiens

<400> 86

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671

```

<210> 87

<400> 87

000

<210> 88

<211> 1108

<212> DNA

<213> Homo sapiens

<400> 88

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```

```

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```

```

<210> 89
<211> 720
<212> DNA
<213> Homo sapiens

```

```
<400> 89
```

```

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```

<210> 90
<211> 837
<212> DNA
<213> Homo sapiens

```

```
<400> 90
```

```

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```

```

<210> 91
<211> 498
<212> DNA
<213> Homo sapiens

```

```
<400> 91
```

```

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```



```

tgacaatgta gaggatgact tctctaata gttacgagct gaactagaga aacatgggta300
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atctgcttgg atttatttgt gtttttgtaa cacaaaaaat aaatgttttg atataaaaag480
gaaagagaaa aattgcgg                                     498

```

```

<210> 92
<211> 1077
<212> DNA
<213> Homo sapiens

```

```
<400> 92
```

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```

```

<210> 93
<211> 1755
<212> DNA
<213> Homo sapiens

```

```
<400> 93
```

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tagtagtagt tctgg

```

1755

&lt;210&gt; 94

&lt;211&gt; 1545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 94

```

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1545

&lt;210&gt; 95

&lt;211&gt; 1133

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 95

```

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atggctgacc aactgactga agagcagatt gcagaattca aagaagcttt ttcactat120
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```

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```

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<210> 96
<211> 791
<212> DNA
<213> Homo sapiens

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<400> 96
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```

```

<210> 97
<211> 599
<212> DNA
<213> Homo sapiens

```

```
<400> 97
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```

```

<210> 98
<211> 643
<212> DNA
<213> Homo sapiens

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<400> 98
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```

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 <211> 860  
 <212> DNA  
 <213> Homo sapiens

<400> 99

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<210> 100  
 <211> 1155  
 <212> DNA  
 <213> Homo sapiens

<400> 100

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```

<210> 101  
 <211> 522  
 <212> DNA  
 <213> Homo sapiens

<400> 101

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```

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```

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<210> 102
<211> 1628
<212> DNA
<213> Homo sapiens

```

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<400> 102

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aaaaaaaaa 1628

```

```

<210> 103
<211> 605
<212> DNA
<213> Homo sapiens

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```

<400> 103

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gggtg 605

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<210> 104
<400> 104

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000

<210> 105  
 <211> 2731  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 105

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2731

<210> 106  
 <211> 2194  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 106

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&lt;210&gt; 107

&lt;211&gt; 1812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

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<210> 108

<211> 890

<212> DNA

<213> Homo sapiens

<400> 108

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<210> 109

<400> 109

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<210> 110

<211> 2627

<212> DNA

<213> Homo sapiens

<400> 110

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<210> 111

<211> 976

<212> DNA

<213> Homo sapiens

<400> 111

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<210> 112

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 112

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&lt;210&gt; 113

&lt;211&gt; 2639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

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<210> 114  
 <211> 634  
 <212> DNA  
 <213> Homo sapiens

<400> 114

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<210> 115  
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 <212> DNA  
 <213> Homo sapiens

<400> 115

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<210> 116  
 <211> 494  
 <212> DNA  
 <213> Homo sapiens

<400> 116

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494

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<210> 117
<211> 1065
<212> DNA
<213> Homo sapiens

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<210> 118
<400> 118
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<210> 119
<400> 119
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<210> 120
<211> 648
<212> DNA
<213> Homo sapiens

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<400> 120
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gcagatctac tactcggaca agtacttcga cgaacactac gactaccggc atgttatggt180
acccagagaa ctttccaaac aagtacctaa aactcatctg atgtctgaag aggagtggag240
gagacttggt gtccaacaga gtctaggctg ggttcattac atgattcatg agccagaacc300
acatattctt ctcttttagac gacctcttcc aaaagatcaa caaaaatgaa gtttatctgg360
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aacagagctc agttaaatgc aactgcaagt aggttactgt aagatgttta agataaaagt540
tcttccagtc agtttttctc ttaagtgcct gtttgagttt actgaaacag tttacttttg600
ttcaataaag tttgtatggt gcatttaaaa aaaaaaaaaa aaagtcga 648

```

```

<210> 121
<211> 1842
<212> DNA
<213> Homo sapiens

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&lt;400&gt; 121

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acttctccaa  gaggggccagg  cactggagta  cgtgtgtcct  tctggcttct  acccgtaccc  120
tgtgcagaca  cgtacctgca  gatctacggg  gtccttgagc  accctgaaga  ctcaagacca  180
aaagactgtc  aggaaggcag  agtgcagagc  aatccactgt  ccaagaccac  acgacttcga  240
gaacggggaa  tactggcccc  ggtctcccta  ctacaatgtg  agtgatgaga  tctctttcca  300
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gtggagtggg  cagacagcga  tctgtgacaa  cggagcgggg  tactgtctca  acccgggcat  420
ccccattggc  acaagggaagg  tgggcagcca  gtaccgcctt  gaagacagcg  tcacctacca  480
ctgcagccgg  gggcttaacc  tgcgtggctc  ccagcggcga  acgtgtcagg  aaggtggctc  540
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ggccgaagct  ttcctgtctt  ccctgacaga  gacctagaa  ggagtcgatg  ctgaggatgg  660
gcacggccca  ggggaacaa  agaagcggaa  gatcgtcctg  gacccttcag  gctccatgaa  720
catctacctg  gtgctagatg  gatcagacag  cattggggcc  agcaacttca  caggagccaa  780
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attgcacaac  atgggcgggg  acccaattac  tgtcattgat  gagatccggg  acttgctata  1140
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ccacaagcaa  ccatggcagg  ccaagatctc  agtcattcgc  ccttcaaagg  gacacgagag  1440
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agaagtagtc  ctatttcacc  ccaactacaa  cattaatggg  aaaaaagaag  caggaattcc  1620
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gactatcagg  cccatttgct  tccccctgcac  cgagggaaca  actcgagctt  tgaggcttcc  1740
tccaactacc  ctttgcagtc  aacaaaaagga  agagctgctc  cccgcagaag  agcaaaagaa  1800
gctgtgtttg  tccgggggga  gaaaaaaacc  gccccggggg  gg  1842

```

&lt;210&gt; 122

&lt;211&gt; 1596

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

```

ggcgggtata  aaagccccac  ccaggccagc  cggctctgct  cagcatttgg  ggaagctctc  60
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agctcagctt  ggagggtgat  cactctacac  ccccaagtgc  atatgggtct  gtcaaagcct  180
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atattgcctt  cgcctaccag  agaaggacca  aaaaggaaat  tgcatcagca  ctgaagtcag  360
ccttatctgg  ccacctggag  acggtgattt  tgggcctatt  gaagacacct  gctcagtatg  420
acgcttctga  gctaaaagct  tccatgaagg  ggctgggaac  cgacgaggac  tctctcattg  480
agatcatctg  ctccagaacc  aaccaggagc  tgcaggaaat  taacagagtc  tacaaggaaa  540
tgtacaagac  tgatctggag  aaggacatta  tttcggacac  atctggtgac  ttccgcaagc  600
tgatggttgc  cctggcaaa  ggtagaagag  cagaggatgg  ctctgtcatt  gattatgaac  660
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ttcccaagtg  gatcagcatc  atgaccgagc  ggagggggcc  cacctccaga  aagtatttga  780
taggtacaag  agttacagcc  cttatgacat  gttggaaaag  atcaggaaa  aggttaaagg  840
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tgctgatcgg  ctgtatgact  ccatgaaggg  caaggggacg  cgagataagg  tcctgatcag  960
aatcatggtc  tcccgagtg  aagtggacat  gttgaaaatt  aggtctgaat  tcaagagaaa  1020
gtacggcaag  tccctgtact  attatatcca  gcaagacact  aagggcgact  accagaaagc  1080
gctgctgtac  ctgtgtggtg  gagatgactg  aagcccgaca  cggcctgagc  gtccgaaaa  1140
gggtgctacc  atgcttccag  ctaacaggtc  tagaaaacca  gcttgcgaa  aacagtcccc  1200
gtggccatcc  ctgtgagggt  gacgttagca  ttaccccaa  cctcatttta  gttgcctaag  1260

```

```

cattgcctgg ccttctgtc tagtctctcc tgtaagccaa agaaatgaac attccaagga1320
gttgggaagt aagtctatga tgtgaaacac tttgcctcct gtgtactgtg tcataaacag1380
atgaataaac tgaatttgta ctttagaaac acgtactttg tggccctgct ttcaactgaa1440
ttgtttgaaa attaaacgtg cttgggggttc agctgggtgag gctgtccctg taggaagaaa1500
gctctggggac tgagctgtac agtatgggtg cccctatcca agtgtcgcta ttttaagttaa1560
atttaaataa aataaaaataa aataaaatca aaaaaa 1596

```

```

<210> 123
<211> 1033
<212> DNA
<213> Homo sapiens

```

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<400> 123
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```

gtgcgagctg accctcgctc ccgccccgc ctggagtcgg acgtggaagt tgctggctga 60
ctgggcttgc gaggaaccgc cctcgagct gcagccgaag gcaaggaatc actgaagatc 120
ggcgaggag gacagggggt tcatcatggg tggctttttc tcaagtatat tttccagtct 180
gtttggaact cgggaaatga gaattttaat tttgggatta gatggagcag gaaaaaccac 240
aattttgtac agattacaag tgggagaagt tggtactact atacctacca ttggatttaa 300
tgtagagacg gtgacgtaca aaaaccttaa attccaagtc tgggatttag gaggacagac 360
aagtatcagg ccatactgga gatgttacta ttcaaacaca gatgcagtca tttatgtagt 420
agacagttgt gaccgagacc gaattggcat ttccaaatca gaggtagttg ccatgttga 480
ggaagaagag ctgagaaaag ccatttttagt ggtgtttgca aataaacagg acatggaaca 540
ggccatgact tcctcagaga tggcaaattc acttgggtta cctgccttga aggaccgaaa 600
atggcagata ttcaaaacgt cagcaaccac aggcaccggc cttgatgagg caatggaatg 660
gttagttgaa acattaaaaa gcagacagta attcagttca ttcttctccc ctgaaatgaa 720
gactacatca cctctctccc tttggaaaac gtcaagtgtg cttcacacta ctagatgtta 780
aaactatatg attattggca tatactgact gactgcaata tttgtagtaa atagggaaaa 840
taagtattta gttggaggga taatttgatc gaatcacctg aatgttctat gtaatgtaaa 900
atattctttt cttgctttct tgtgttaagg tatatattct atttgtatgg aattcttatt 960
caaatacagt tctattaaag agtatactcc tattggatga aaaaaaccta aaaaaaaaaa1020
aaaaaaaaaa aaa 1033

```

```

<210> 124
<211> 65
<212> PRT
<213> Homo sapiens

```

```
<400> 124
```

```

Ile  Cys  Leu  Leu  Val  His  Phe  Val  Ser  Arg  Ala  Lys  Thr  Val  Asn  Leu
  1      5      10      15
Thr  Phe  Ser  Tyr  Trp  Trp  Val  Ile  Thr  Glu  Asn  Lys  Asp  Leu  Phe  Ser
      20      25      30
Cys  Ser  Leu  Leu  Lys  Ser  His  Lys  Asn  Asn  Gln  Ile  Gly  Ser  Cys  Leu
      35      40      45
Leu  Ser  Cys  Val  Ser  Trp  Phe  Leu  Thr  Cys  Val  His  Thr  Pro  Val  Cys
      50      55      60
Leu
65

```

```

<210> 125
<211> 64
<212> PRT
<213> Homo sapiens

```

```
<400> 125
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```
Ile  Ser  Val  Phe  Arg  Leu  Phe  Lys  Tyr  Leu  Thr  His  Phe  Gln  Thr  Cys
```

1	5							10					15			
Thr	Met	Phe	Tyr 20	Lys	Pro	Leu	Asp	Phe 25	Gln	Gln	His	Thr	Ile 30	Glu	Asn	
Thr	Cys	Tyr 35	Ser	Lys	His	Asn	Phe 40	Ser	Val	Ser	Ser	Ile 45	Ala	Val	Val	
Arg	Asp 50	Asn	Ile	Ala	Ile	Ser 55	Gly	Met	Leu	Gln	Ala 60	Phe	Lys	Ile	Ala	

<210> 126  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 126

Lys 1	Ala	Asn	Leu	Leu 5	Pro	Ala	Thr	Pro	Glu 10	Gly	Thr	Gln	Ile	Trp 15	Val
Gly	Pro	Val	Phe 20	Gln	Leu	Gly	Lys	Arg 25	Met	Gly	Lys	Pro	Gly 30	Asp	Gly
Phe	His	Lys 35	Phe	Ser	Ser	Gly	Leu 40	Trp	His	Ser	Phe	Gln 45	Glu	Ile	Pro
Leu	Gly 50	Lys	Gly	Leu	Leu	Ala 55	Asn	Met	His	Phe	Gln 60	Thr			

<210> 127  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 127

Leu 1	Lys	Asn	Thr	Asn 5	Glu	Val	Lys	Ala	Leu 10	Asn	Trp	Tyr	Thr	Leu 15	Phe
Thr	Pro	Ile	Phe 20	Gln	Val	Trp	Lys	Cys 25	Ile	Phe	Ala	Ser	Arg 30	Pro	Leu
Pro	Arg	Gly 35	Ile	Ser	Trp	Lys	Glu 40	Cys	His	Asn	Pro	Leu 45	Glu	Asn	Leu
Trp	Lys 50	Pro	Ser	Pro	Gly	Phe 55	Pro	Ile	Arg	Leu	Pro 60	Ser	Trp	Lys	Thr
Gly 65	Pro	Thr	His	Ile	Trp 70	Val	Pro	Ser	Gly	Val 75	Ala	Gly	Arg	Arg	Phe 80
Ala	Phe														

<210> 128  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 128

His 1	Thr	Trp	Asp	Pro 5	Tyr	Pro	Leu	Gly	Ile 10	Ser	Pro	Arg	Thr	Ile 15	Arg
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Pro	Val	Cys	Gln 20	Pro	Lys	Val	Ala	Phe 25	Gly	Met	Leu	Asn	Phe 30	Pro	Leu
Ser	Lys	Lys 35	Val	His	Leu	Pro	Asn 40	Glu	Val	Thr	Ile	Arg 45	Leu	Asn	Pro
Lys	Lys 50	Ser	Leu	Asp	Phe	Val 55	Phe	Tyr	Lys	Asn	Ser 60	Thr	Phe	Pro	Ile
Lys 65	Ser	Leu	Val	Ile	Lys 70	Ile	Ser	Thr	Leu	Pro 75	Lys	Cys	Asp	Ser	Thr 80
Ala	Trp	Phe	Leu	Ala 85	Asn	Lys	Asn	Pro	Ile 90						

&lt;210&gt; 129

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 129

Met 1	Val	Ala	Asp	Tyr 5	Gly	Cys	Thr	Ile	Leu 10	Ile	Leu	Gly	Pro	Phe 15	Thr
His	Arg	Asn	His 20	Thr	Lys	Trp	Pro	Asp 25	Thr	Tyr	Phe	Thr	Glu 30	Gln	Phe
Lys	Tyr	Tyr 35	Thr	Leu	Ala	Lys	Ser 40	Thr	Tyr	Ser	Thr	His 45	Pro	Gly	Glu
Gly	Gly 50	Glu	Lys	Thr	His	Thr 55	Tyr	Lys	Thr	Thr	Ser 60	Leu	Asp	Thr	Met
Cys 65	Leu	Pro	Thr	Ile	Ser 70	Ser	Leu	Asn	Asn	Phe 75	His	Gln	Leu	Arg	Cys 80
Leu	Val														

&lt;210&gt; 130

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

Arg 1	Asn	Leu	Val	Thr 5	Gln	Met	Lys	Ser	Gly 10	Ile	Glu	Asp	Pro	Trp 15	Thr
Trp	Gln	Val	Asn 20	Ala	Asp	Tyr	Ser	Leu 25	Ala	Phe	Pro	Leu	Tyr 30	Leu	Cys
Lys	Glu	Gly 35	Tyr	Thr	Glu	Leu	Ile 40	Leu	Phe	Gln	Ala	Tyr 45	Asn	Phe	Lys
Phe	Tyr 50	His	Leu	Asn	Ser	Ser 55	Thr	Phe	Ala	Ala	Glu 60	Glu	Trp	Asn	Gln
Lys 65	Asn	Val	Val	Ser	Trp 70										

&lt;210&gt; 131



<211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 131

Ala	Ile	Gln	Cys	Glu	Ala	Tyr	Phe	Ile	Ala	Thr	Leu	Val	Asp	Cys	Gln
1				5					10					15	
Gly	Asp	Ser	Ala	Thr	Val	Leu	Asp	Lys	Leu	Met	Phe	Pro	Phe	Ser	Leu
			20					25					30		
Ala	Ala	Asn	Arg	Arg	Ala	Thr	Tyr	Ser	Ala	Gly	Ser	Arg	Ala	Arg	Ser
		35					40					45			
Trp	Gly	Ser	Arg	Gly	Tyr	Thr	Ser	Ser	Leu	Ile	Ile				
	50					55					60				

<210> 132  
 <211> 181  
 <212> PRT  
 <213> Homo sapiens

<400> 132

Ile	Pro	Asn	Met	Ala	Ala	Pro	Leu	Gly	Gly	Met	Phe	Ser	Gly	Gln	Pro
1				5					10					15	
Pro	Gly	Pro	Pro	Gln	Ala	Pro	Pro	Gly	Leu	Pro	Gly	Gln	Ala	Ser	Leu
			20					25					30		
Leu	Gln	Ala	Ala	Pro	Gly	Ala	Pro	Arg	Pro	Ser	Ser	Ser	Thr	Leu	Val
		35					40					45			
Asp	Glu	Leu	Glu	Ser	Ser	Phe	Glu	Ala	Cys	Phe	Ala	Ser	Leu	Val	Ser
	50					55					60				
Gln	Asp	Tyr	Val	Asn	Gly	Thr	Asp	Gln	Glu	Glu	Ile	Arg	Thr	Gly	Val
65					70					75					80
Asp	Gln	Cys	Ile	Gln	Lys	Phe	Leu	Asp	Ile	Ala	Arg	Gln	Thr	Glu	Cys
				85					90					95	
Phe	Phe	Leu	Gln	Lys	Arg	Leu	Gln	Leu	Ser	Val	Gln	Lys	Pro	Glu	Gln
			100					105					110		
Val	Ile	Lys	Glu	Asp	Val	Ser	Glu	Leu	Arg	Asn	Glu	Leu	Gln	Arg	Lys
		115					120					125			
Asp	Ala	Leu	Val	Gln	Lys	His	Leu	Thr	Lys	Leu	Arg	His	Trp	Gln	Gln
	130					135					140				
Val	Leu	Glu	Asp	Ile	Asn	Val	Gln	His	Lys	Lys	Pro	Ala	Asp	Ile	Pro
145					150					155					160
Gln	Gly	Ser	Leu	Ala	Tyr	Leu	Glu	Gln	Ala	Ser	Ala	Asn	Ile	Pro	Ala
				165					170					175	
Pro	Leu	Lys	Pro	Thr											
			180												

<210> 133  
 <211> 423

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

Leu 1	Ser	Glu	Asp	Glu 5	Ile	Arg	Thr	Leu	Lys 10	Gln	Lys	Lys	Ile	Asp 15	Glu
Thr	Ser	Glu	Gln 20	Glu	Gln	Lys	His	Lys 25	Glu	Thr	Asn	Asn	Ser 30	Asn	Ala
Gln	Asn	Pro 35	Ser	Glu	Glu	Glu	Gly 40	Glu	Gly	Gln	Asp	Glu 45	Asp	Ile	Leu
Pro	Leu 50	Thr	Leu	Glu	Glu	Lys 55	Glu	Asn	Lys	Glu	Tyr 60	Leu	Lys	Ser	Leu
Phe 65	Glu	Ile	Leu	Ile	Leu 70	Met	Gly	Lys	Gln	Asn 75	Ile	Pro	Leu	Asp	Gly 80
His	Glu	Ala	Asp	Glu 85	Ile	Pro	Glu	Gly	Leu 90	Phe	Thr	Pro	Asp	Asn 95	Phe
Gln	Ala	Leu	Leu 100	Glu	Cys	Arg	Ile	Asn 105	Ser	Gly	Glu	Glu	Val 110	Leu	Arg
Lys	Arg	Phe 115	Glu	Thr	Thr	Ala	Val 120	Asn	Thr	Leu	Phe	Cys 125	Ser	Lys	Thr
Gln	Gln 130	Arg	Gln	Met	Leu	Glu 135	Ile	Cys	Glu	Ser	Cys 140	Ile	Arg	Glu	Glu
Thr 145	Leu	Arg	Glu	Val	Arg 150	Asp	Ser	His	Phe	Phe 155	Ser	Ile	Ile	Thr	Asp 160
Asp	Val	Val	Asp	Ile 165	Ala	Gly	Glu	Glu	His 170	Leu	Pro	Val	Leu	Val 175	Arg
Phe	Val	Asp	Glu 180	Ser	His	Asn	Leu	Arg 185	Glu	Glu	Phe	Ile	Gly 190	Phe	Leu
Pro	Tyr	Glu 195	Ala	Asp	Ala	Glu	Ile 200	Leu	Ala	Val	Lys	Phe 205	His	Thr	Met
Ile	Thr 210	Glu	Lys	Trp	Gly	Leu 215	Asn	Met	Glu	Tyr	Cys 220	Arg	Gly	Gln	Ala
Tyr 225	Ile	Val	Ser	Ser	Gly 230	Phe	Ser	Ser	Lys	Met 235	Lys	Val	Val	Ala	Ser 240
Arg	Leu	Leu	Glu	Lys 245	Tyr	Pro	Gln	Ala	Ile 250	Tyr	Thr	Leu	Cys	Ser 255	Ser
Cys	Ala	Leu	Asn 260	Met	Trp	Leu	Ala	Lys 265	Ser	Val	Pro	Val	Met 270	Gly	Val
Ser	Val	Ala 275	Leu	Gly	Thr	Ile	Glu 280	Glu	Val	Cys	Ser	Phe 285	Phe	His	Arg
Ser	Pro 290	Gln	Leu	Leu	Leu	Glu 295	Leu	Asp	Asn	Val	Ile 300	Ala	Val	Leu	Phe
Gln	Asn	Ser	Lys	Glu	Arg	Gly	Lys	Glu	Leu	Lys	Glu	Ile	Cys	His	Ser

305					310					315					320
Gln	Trp	Thr	Gly	Arg	His	Asp	Ala	Phe	Glu	Ile	Leu	Val	Glu	Leu	Leu
				325					330					335	
Gln	Ala	Leu	Val	Leu	Cys	Leu	Asp	Gly	Ile	Asn	Ser	Asp	Thr	Asn	Ile
			340					345					350		
Arg	Trp	Asn	Asn	Tyr	Ile	Ala	Gly	Arg	Ala	Phe	Val	Leu	Cys	Ser	Ala
		355					360					365			
Val	Ser	Asp	Phe	Asp	Phe	Ile	Val	Thr	Ile	Val	Val	Leu	Lys	Asn	Val
	370					375					380				
Leu	Ser	Phe	Thr	Arg	Ala	Phe	Gly	Lys	Asn	Leu	Gln	Gly	Gln	Thr	Ser
385					390					395					400
Asp	Val	Phe	Phe	Ala	Ala	Gly	Ser	Leu	Thr	Ala	Val	Leu	His	Ser	Leu
				405					410					415	
Asn	Glu	Val	Ser	Gly	Lys	Tyr									
			420												

&lt;210&gt; 134

&lt;211&gt; 237

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

Val	Glu	Asn	Ile	Glu	Val	Tyr	His	Glu	Phe	Trp	Phe	Glu	Glu	Ala	Thr
1				5				10						15	
Asn	Leu	Ala	Thr	Lys	Leu	Asp	Ile	Gln	Met	Lys	Leu	Pro	Gly	Lys	Phe
			20					25					30		
Arg	Arg	Ala	His	Gln	Gly	Asn	Leu	Glu	Ser	Gln	Leu	Thr	Ser	Glu	Ser
		35					40					45			
Tyr	Tyr	Lys	Glu	Thr	Leu	Ser	Val	Pro	Thr	Val	Glu	His	Ile	Ile	Gln
	50					55					60				
Glu	Leu	Lys	Asp	Ile	Phe	Ser	Glu	Gln	His	Leu	Lys	Ala	Leu	Lys	Cys
65					70					75					80
Leu	Ser	Leu	Val	Pro	Ser	Val	Met	Gly	Gln	Leu	Lys	Phe	Asn	Thr	Ser
				85					90					95	
Glu	Glu	His	His	Ala	Asp	Met	Tyr	Arg	Ser	Asp	Leu	Pro	Asn	Pro	Asp
			100					105					110		
Thr	Leu	Ser	Ala	Glu	Leu	His	Cys	Trp	Arg	Ile	Lys	Trp	Lys	His	Arg
		115					120					125			
Gly	Lys	Asp	Ile	Glu	Leu	Pro	Ser	Thr	Ile	Tyr	Glu	Ala	Leu	His	Leu
	130					135					140				
Pro	Asp	Ile	Lys	Phe	Phe	Pro	Asn	Val	Tyr	Ala	Leu	Leu	Lys	Val	Leu
145					150					155					160
Cys	Ile	Leu	Pro	Val	Met	Lys	Val	Glu	Asn	Glu	Arg	Tyr	Glu	Asn	Gly
				165					170					175	

Arg	Lys	Arg	Leu 180	Lys	Ala	Tyr	Leu	Arg 185	Asn	Thr	Leu	Thr	Asp 190	Gln	Arg
Ser	Ser	Asn 195	Leu	Ala	Leu	Leu	Asn 200	Ile	Asn	Phe	Asp	Ile 205	Lys	His	Asp
Leu	Asp 210	Leu	Met	Val	Asp	Thr 215	Tyr	Ile	Lys	Leu	Tyr 220	Thr	Ser	Lys	Ser
Glu 225	Leu	Pro	Thr	Asp	Asn 230	Ser	Glu	Thr	Val	Glu 235	Asn	Thr			

&lt;210&gt; 135

&lt;211&gt; 89

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 135

Arg 1	Ile	Arg	Ile	Asn 5	Gly	Ser	Leu	Cys	Pro 10	Gln	Thr	Lys	Asn	Asn 15	Leu
Tyr	Phe	His	Ile 20	Val	Glu	Leu	Ser	Ile 25	Ser	Gly	Ala	Ser	Val 30	Gly	Glu
Arg	Trp	Tyr 35	Gly	Met	Gly	Glu	Ser 40	Ile	Leu	Pro	Ala	Arg 45	Gly	Glu	Ser
Gln	Gly 50	Leu	Leu	Cys	Leu	Tyr 55	Phe	Tyr	Lys	Glu	Ile 60	Leu	Pro	Leu	Phe
Leu 65	Val	Asn	Lys	Leu	Arg 70	Gly	Thr	Asp	Val	Gly 75	Leu	Glu	Gln	Gly	Leu 80
Ser	Gly	Gly	Glu	Gly 85	Ser	Trp	Thr	Ala							

&lt;210&gt; 136

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

Glu 1	Glu	Glu	Arg	Ala 5	Lys	Arg	Glu	Glu	Leu 10	Arg	Ile	Leu	Glu 15	Glu	
Asn	Asn	Arg	Lys 20	Ile	Ala	Glu	Ala	Gln 25	Ala	Lys	Leu	Ala	Glu 30	Glu	Gln
Leu	Arg	Ile 35	Val	Glu	Glu	Gln	Arg 40	Lys	Ile	His	Glu	Glu 45	Arg	Met	Lys
Leu	Glu 50	Gln	Glu	Arg	Gln	Arg 55	Gln	Gln	Lys	Glu	Glu 60	Gln	Lys	Ile	Ile
Leu 65	Gly	Lys	Gly	Lys	Ser 70	Arg	Pro	Lys	Leu	Ser 75	Phe	Ser	Leu	Lys	Thr 80
Gln	Asp														

&lt;210&gt; 137

&lt;211&gt; 71

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

Ser	Ala	Leu	Lys	Val	Glu	Tyr	Leu	Leu	Ser	Cys	Pro	Val	Ser	Cys	Arg
1				5					10					15	
Val	Cys	Ser	Ser	Ala	Ala	Ile	Arg	Ala	Ser	Phe	Leu	Phe	Lys	Met	Ile
			20					25					30		
Cys	Thr	Val	Ser	Leu	Ala	Ile	Pro	Ala	Ser	Ala	Ala	Gln	Pro	Phe	Ile
		35					40					45			
Lys	Lys	Gln	His	Thr	Arg	Lys	Ala	Glu	Leu	Arg	Asn	Ala	Asp	Val	Tyr
	50					55					60				
Gly	Lys	Lys	Glu	Gln	Lys	Met									
65					70										

&lt;210&gt; 138

&lt;211&gt; 67

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

Ser	Ser	Ala	Gln	Arg	Lys	Tyr	Phe	Asn	Leu	Pro	Val	Glu	Ile	Leu	Val
1				5					10					15	
Met	Glu	Arg	Cys	Gln	Thr	Val	Leu	Asn	Gly	Arg	Thr	Ser	Lys	Ser	Glu
			20					25					30		
Ala	Thr	Val	Pro	Thr	Thr	Arg	Gly	Leu	Leu	Tyr	Cys	Ser	Thr	Phe	Ser
		35					40					45			
Ala	Leu	Tyr	Phe	Leu	Ala	Glu	Ala	Ser	Pro	Trp	Ser	Ala	Met	Tyr	Lys
	50					55					60				
Leu	Gly	Tyr													
65															

&lt;210&gt; 139

&lt;211&gt; 49

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

Arg	Ala	Glu	Lys	Val	Glu	Gln	Tyr	Lys	Ser	Pro	Arg	Val	Val	Gly	Thr
1				5					10					15	
Val	Ala	Ser	Leu	Leu	Leu	Val	Leu	Pro	Phe	Lys	Thr	Val	Trp	His	Leu
			20					25					30		
Ser	Met	Thr	Arg	Ile	Ser	Thr	Gly	Arg	Leu	Lys	Tyr	Phe	Leu	Cys	Ala
		35					40					45			
Glu															

&lt;210&gt; 140

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

Ser	Cys	Glu	Arg	Arg	Gly	Phe	Ile	Met	Ala	Asp	Asp	Leu	Lys	Arg	Phe
1				5					10					15	
Leu	Tyr	Lys	Lys	Leu	Pro	Ser	Val	Glu	Gly	Leu	His	Ala	Ile	Val	Val
			20					25					30		
Ser	Asp	Arg	Asp	Gly	Val	Pro	Val	Ile	Lys	Val	Ala	Asn	Asp	Asn	Ala
		35					40					45			
Pro	Glu	His	Ala	Leu	Arg	Pro	Gly	Phe	Leu	Ser	Thr	Phe	Ala	Leu	Ala
	50					55					60				
Thr	Asp	Gln	Gly	Ser	Lys	Leu	Gly	Leu	Ser	Lys	Asn	Lys	Ser	Ile	Ile
65					70					75					80
Cys	Tyr	Tyr	Asn	Thr	Tyr	Gln	Val	Val	Gln	Phe	Asn	Arg	Leu	Pro	Leu
				85					90					95	
Val	Val	Ser	Phe	Ile	Ala	Ser	Ser	Ser	Ala	Asn	Thr	Gly	Leu	Ile	Val
			100					105					110		
Ser	Leu	Glu	Lys	Glu	Leu	Ala	Pro	Leu	Phe	Glu	Glu	Leu	Arg	Gln	Val
		115					120					125			
Val	Glu	Val	Ser												
	130														

&lt;210&gt; 141

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

Gln	Met	Ile	Leu	Leu	Phe	Leu	Glu	Ser	Pro	Ser	Leu	Leu	Pro	Trp	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Lys	Val	Asp	Lys	Lys	Pro	Gly	Arg	Lys	Ala	Cys	Ser
			20					25					30		
Gly	Ala	Leu	Ser	Phe	Ala	Thr	Leu	Ile	Thr	Gly	Thr	Pro	Ser	Leu	Ser
		35					40					45			
Asp	Thr	Thr	Met	Ala	Trp	Ser	Pro	Ser	Thr	Leu	Gly	Asn	Phe	Leu	Tyr
	50					55					60				
Lys	Asn	Arg	Phe	Arg	Ser	Ser	Ala	Met	Met	Asn	Pro	Leu	Leu	Ser	Gln
65					70					75					80
Asp	Gln	Ser	Pro	Arg	Leu	Gly	Phe	Leu	Gly	Cys	Leu	Val	Leu	Ser	Ala
				85					90					95	
Val	Thr	Ser	Gly	Thr	Ala	Leu	Lys	Thr	Gly	Ser	Ser	Ser	Ser	His	Arg
			100					105					110		
His	Met	Ile	His	Asp	Leu	Val	Cys	Ala	Pro	Gly	Ser	Thr	Phe		
		115					120					125			

&lt;210&gt; 142

<211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 142

Ser 1	Ala	Val	Lys	Arg 5	Gly	Trp	Asp	Leu	Asn 10	Met	Ala	Ala	Val	Val 15	Ala
Ala	Thr	Ala	Leu 20	Lys	Gly	Arg	Gly	Ala 25	Arg	Asn	Ala	Arg	Val 30	Leu	Arg
Gly	Ile	Leu 35	Ala	Gly	Ala	Thr	Ala 40	Asn	Lys	Ala	Ser	His 45	Asn	Arg	Thr
Arg	Ala 50	Leu	Gln	Ser	His	Ser 55	Ser	Pro	Glu	Gly	Lys 60	Glu	Glu	Pro	Glu
Pro 65	Leu	Ser	Pro	Glu	Leu 70	Glu	Tyr	Ile	Pro	Arg 75	Lys	Arg	Gly	Lys	Asn 80
Pro	Met	Lys	Ala	Val 85	Gly	Leu	Ala	Trp	Ala 90	Ile	Gly	Phe	Pro	Cys 95	Gly
Ile	Leu	Leu	Phe 100	Ile	Leu	Thr	Lys	Arg 105	Glu	Val	Asp	Lys	Asp 110	Arg	Val
Lys	Gln	Met 115	Lys	Ala	Arg	Gln	Asn 120	Met	Arg	Leu	Ser	Asn 125	Thr	Gly	Glu
Tyr	Glu 130	Ser	Gln	Arg	Phe	Arg 135	Ala	Ser	Ser	Gln	Ser 140	Ala	Pro	Ser	Pro
Asp 145	Val	Gly	Ser	Gly	Val 150	Gln	Thr								

<210> 143  
 <211> 114  
 <212> PRT  
 <213> Homo sapiens

<400> 143

Glu 1	Gly	Arg	Ser	Ala 5	Pro	Gln	Val	Cys	Thr 10	Pro	Asp	Pro	Thr	Ser 15	Gly
Asp	Gly	Ala	Leu 20	Trp	Glu	Glu	Ala	Leu 25	Asn	Leu	Trp	Leu	Ser 30	Tyr	Ser
Pro	Val	Leu 35	Asp	Asn	Arg	Met	Phe 40	Cys	Arg	Ala	Phe	Ile 45	Cys	Phe	Thr
Arg	Ser 50	Leu	Ser	Thr	Ser	Arg 55	Leu	Val	Arg	Met	Lys 60	Arg	Arg	Ile	Pro
Gln 65	Gly	Lys	Pro	Met	Ala 70	Gln	Ala	Ser	Pro	Thr 75	Ala	Phe	Met	Gly	Phe 80
Leu	Pro	Leu	Phe	Leu 85	Gly	Met	Tyr	Ser	Ser 90	Ser	Gly	Asp	Arg	Gly 95	Ser
Gly	Ser	Ser	Leu 100	Pro	Ser	Gly	Glu	Leu 105	Trp	Leu	Cys	Arg	Ala 110	Arg	Val

Leu Leu

<210> 144

<211> 267

<212> PRT

<213> Homo sapiens

<400> 144

Glu 1	Asp	Glu	Val	Glu 5	Glu	Glu	Ser	Thr	Ala 10	Leu	Gln	Lys	Thr	Asp 15	Lys
Lys	Glu	Ile	Leu 20	Lys	Lys	Ser	Glu	Lys 25	Asp	Thr	Asn	Ser	Lys 30	Val	Lys
Pro	Lys	Gly 35	Lys	Val	Arg	Trp	Thr 40	Gly	Ser	Arg	Thr	Arg 45	Gly	Arg	Trp
Lys	Tyr 50	Ser	Ser	Asn	Asp	Glu 55	Ser	Glu	Gly	Ser	Gly 60	Ser	Glu	Lys	Ser
Ser 65	Ala	Ala	Ser	Glu	Glu 70	Glu	Glu	Glu	Lys	Glu 75	Ser	Glu	Glu	Ala	Ile 80
Leu	Ala	Asp	Asp	Asp 85	Glu	Pro	Cys	Lys	Lys 90	Cys	Gly	Leu	Pro	Asn 95	His
Pro	Glu	Leu	Ile 100	Leu	Leu	Cys	Asp	Ser 105	Cys	Asp	Ser	Gly	Tyr 110	His	Thr
Ala	Cys	Leu 115	Arg	Pro	Pro	Leu	Met 120	Ile	Ile	Pro	Asp	Gly 125	Glu	Trp	Phe
Cys	Pro 130	Pro	Cys	Gln	His	Lys 135	Leu	Leu	Cys	Glu	Lys 140	Leu	Glu	Glu	Gln
Leu 145	Gln	Asp	Leu	Asp	Val 150	Ala	Leu	Lys	Lys	Lys 155	Glu	Arg	Ala	Glu	Arg 160
Arg	Lys	Glu	Arg	Leu 165	Val	Tyr	Val	Gly	Ile 170	Ser	Ile	Glu	Asn	Ile 175	Ile
Pro	Pro	Gln	Glu 180	Pro	Asp	Phe	Ser	Glu 185	Asp	Gln	Glu	Glu	Lys 190	Lys	Lys
Asp	Ser	Lys 195	Lys	Ser	Lys	Ala	Asn 200	Leu	Leu	Glu	Arg	Arg 205	Ser	Thr	Arg
Thr	Arg 210	Lys	Cys	Ile	Ser	Tyr 215	Arg	Phe	Asp	Glu	Phe 220	Asp	Glu	Ala	Ile
Asp 225	Glu	Ala	Ile	Glu	Asp 230	Asp	Ile	Lys	Glu	Ala 235	Asp	Gly	Gly	Gly	Val 240
Gly	Arg	Gly	Lys	Asp 245	Ile	Ser	Thr	Ile	Thr 250	Gly	His	Arg	Gly	Lys 255	Asp
Ile	Ser	Thr	Ile 260	Leu	Asp	Glu	Lys	Ile 265	Ile	Thr					

<210> 145

<211> 185



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 145

Ser 1	Ser	Glu	Lys	Ser 5	Gly	Ser	Cys	Gly	Gly 10	Met	Met	Phe	Ser	Ile 15	Leu
Ile	Pro	Thr	Tyr 20	Thr	Lys	Arg	Ser	Phe 25	Leu	Arg	Ser	Ala	Arg 30	Ser	Phe
Phe	Phe	Lys 35	Ala	Thr	Ser	Lys	Ser 40	Cys	Asn	Cys	Ser	Ser 45	Asn	Phe	Ser
Gln	Ser 50	Ser	Leu	Cys	Trp	Gln 55	Gly	Gly	Gln	Asn	His 60	Ser	Pro	Ser	Gly
Met 65	Ile	Ile	Arg	Gly	Gly 70	Arg	Arg	Gln	Ala	Val 75	Trp	Tyr	Pro	Leu	Ser 80
Gln	Glu	Ser	His	Arg 85	Arg	Ile	Ser	Ser	Gly 90	Trp	Phe	Gly	Arg	Pro 95	His
Phe	Leu	His	Gly 100	Ser	Ser	Ser	Ser	Ala 105	Arg	Met	Ala	Ser	Ser 110	Leu	Ser
Phe	Ser	Ser 115	Ser	Ser	Ser	Glu	Ala 120	Ala	Asp	Asp	Phe	Ser 125	Leu	Pro	Asp
Pro	Ser 130	Leu	Ser	Ser	Leu	Leu 135	Glu	Tyr	Phe	His	Leu 140	Pro	Arg	Val	Arg
Glu 145	Pro	Val	His	Arg	Thr 150	Leu	Pro	Leu	Gly	Phe 155	Thr	Leu	Glu	Phe	Val 160
Ser	Phe	Ser	Asp	Phe 165	Phe	Lys	Ile	Ser	Phe 170	Leu	Ser	Val	Phe	Cys 175	Lys
Ala	Val	Asp	Ser 180	Ser	Ser	Thr	Ser	Ser 185							

&lt;210&gt; 146

&lt;400&gt; 146

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&lt;210&gt; 147

&lt;400&gt; 147

000

&lt;210&gt; 148

&lt;211&gt; 134

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

Lys 1	Arg	Gln	Pro	Thr 5	Ser	Ala	Met	Lys	Asp 10	Pro	Ser	Arg	Ser	Ser 15	Thr
Ser	Pro	Ser	Ile 20	Ile	Asn	Glu	Asp	Val 25	Ile	Ile	Asn	Gly	His 30	Ser	His
Glu	Asp	Asp	Asn	Pro	Phe	Ala	Glu	Tyr	Met	Trp	Met	Glu	Asn	Glu	Glu

35						40					45				
Glu	Phe	Asn	Arg	Gln	Ile	Glu	Glu	Glu	Leu	Trp	Glu	Glu	Glu	Phe	Ile
	50					55					60				
Glu	Arg	Cys	Phe	Gln	Glu	Met	Leu	Glu	Glu	Glu	Glu	Glu	His	Glu	Trp
65					70					75					80
Phe	Ile	Pro	Ala	Arg	Asp	Leu	Pro	Gln	Thr	Met	Asp	Gln	Ile	Gln	Asp
				85					90					95	
Gln	Phe	Asn	Asp	Leu	Val	Ile	Ser	Asp	Gly	Ser	Ser	Leu	Glu	Asp	Leu
			100					105					110		
Val	Val	Lys	Ser	Asn	Leu	Asn	Pro	Asn	Ala	Lys	Glu	Phe	Val	Pro	Gly
		115					120					125			
Val	Lys	Tyr	Gly	Asn	Ile										
	130														

&lt;210&gt; 149

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 149

His	Ser	Asp	Lys	Arg	Ala	Phe	Thr	Ile	Lys	Ser	Ser	Asn	Thr	Ala	Phe
1				5					10					15	
Thr	Val	Trp	Lys	Leu	Cys	Tyr	Ile	His	Gln	Lys	Arg	Ala	Pro	Ser	Thr
			20					25					30		
Gln	Ile	Phe	Pro	Tyr	Phe	Thr	Pro	Gly	Thr	Asn	Ser	Phe	Ala	Phe	Gly
		35					40					45			
Phe	Arg	Leu	Leu	Leu	Thr	Thr	Arg	Ser	Ser	Arg	Glu	Glu	Pro	Ser	Leu
	50					55					60				
Ile	Thr	Arg	Ser	Leu	Asn	Trp	Ser	Trp	Ile	Trp	Ser	Ile	Val	Cys	Gly
65					70					75					80
Arg	Ser	Arg	Ala	Gly	Ile	Asn	His	Ser	Cys	Ser	Ser	Ser	Ser	Ser	Ser
				85					90					95	
Ile	Ser	Trp	Lys	Gln	Arg	Ser	Ile	Asn	Ser	Ser	Ser	His	Asn	Ser	Ser
			100					105					110		
Ser	Ile	Cys	Leu	Leu	Asn	Ser	Ser	Ser	Phe	Ser	Ile	His	Met	Tyr	Ser
		115					120					125			
Ala	Asn	Gly	Leu	Ser	Ser	Ser									
	130						135								

&lt;210&gt; 150

&lt;211&gt; 58

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

Leu	Val	Ser	Gly	Ala	Asn	Gln	Cys	Gly	Ser	Cys	Asn	Ser	Lys	Ser	Phe
1				5					10					15	

Leu	Thr	Lys	Ala 20	Trp	Tyr	Tyr	Arg	Val 25	Gly	Phe	Arg	Phe	Phe 30	Arg	Gly	
Gly	Leu	Phe 35	Asp	Phe	Asp	Phe	Phe 40	Phe	Phe	Tyr	Val	Ile 45	Phe	Gly	Lys	
Thr	His 50	Ser	Glu	Leu	Tyr	Leu 55	Val	Ser	Thr							

<210> 151  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 151

Phe 1	Phe	Val	Leu	Lys 5	Ser	Leu	Leu	Val	Gly 10	Ala	Cys	Tyr	Trp	Glu 15	Gln	
Val	Phe	Val	Gln 20	Lys	Leu	Gln	Ser	Glu 25	Ser	Leu	Cys	Ile	Thr 30	Glu	Thr	
Leu	Phe	Ile 35	Thr	Ser	Leu	Leu	Ser 40	Leu	Pro	Gln	Lys	Thr 45	Val	Gly	Leu	
Asn	Lys 50	Ile	Ile	Cys	Ile	Leu 55	Ile	Tyr	Leu	Lys	Cys 60	Leu				

<210> 152  
 <211> 60  
 <212> PRT  
 <213> Homo sapiens

<400> 152

Ser 1	Ala	Cys	Lys	Phe 5	Leu	Arg	Asp	Leu	Pro 10	Leu	Leu	Thr	Val	Asp 15	Gln	
Leu	Met	Tyr	Thr 20	Cys	Ile	Ile	Lys	Ala 25	Leu	Asn	Lys	Ser	Leu 30	Trp	Leu	
Ile	Thr	Ala 35	Lys	Met	Gly	Thr	Arg 40	His	Leu	Leu	Cys	Val 45	Leu	Val	Thr	
Ala	Val 50	Ala	Leu	Arg	Ala	Val 55	Arg	Pro	Cys	Leu	Ile 60					

<210> 153  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 153

Lys 1	Arg	Asp	Ile	Ile 5	Leu	Asn	Val	Phe	Ser 10	Gln	Arg	Ser	His	Lys 15	Arg	
Lys	Lys	Asn	Gln 20	Asn	Gln	Ile	Asn	His 25	His	Glu	Lys	Asn	Glu 30	Thr	Pro	
His	Gly	Asn 35	Thr	Lys	Leu	Trp	Leu 40	Gly	Ser	Ser	Tyr	Tyr 45	Tyr	Ser	Ser	

His Ile Gly Trp Arg Arg Lys Pro  
50 55

<210> 154  
<400> 154  
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<210> 155  
<211> 150  
<212> PRT  
<213> Homo sapiens

<400> 155

Ile	Pro	Val	His	Arg	Leu	His	Gly	Arg	Ala	Asp	Pro	Leu	Gly	Trp	Ser
1				5					10					15	
Ile	Val	Ser	Asp	Leu	Ile	Thr	Ser	Gly	Leu	Gly	Ala	Gly	Val	Leu	Arg
			20					25					30		
Gly	Leu	Pro	Ala	Arg	Arg	Leu	His	Ser	Leu	Gly	Arg	Arg	Val	Leu	Gly
		35					40					45			
Arg	Pro	Gly	Val	Trp	Leu	Glu	Arg	Leu	Gly	His	Gly	Arg	Arg	Asp	Ala
	50					55					60				
Leu	Gly	Ala	Trp	Ser	Ala	Ala	Gln	Arg	Pro	Arg	Thr	Pro	Gly	Arg	Pro
65					70					75					80
Ala	Cys	Val	Cys	Ala	Pro	Arg	Arg	Gly	Pro	Glu	Ser	Pro	Ser	Ala	Asp
				85					90					95	
Pro	Val	Pro	Pro	Pro	Gly	Arg	Ala	Gly	Asp	Pro	Ser	Pro	Pro	Asp	Ala
			100					105					110		
Ser	Ala	Ser	Gly	Pro	Arg	Gly	Gly	Ala	Ala	Thr	Lys	Ala	Gly	Pro	Ala
		115					120					125			
His	Asp	Pro	Gly	Gln	Leu	Arg	Pro	Glu	Leu	Arg	Val	Leu	Pro	Pro	Pro
	130					135					140				
Pro	Arg	Gly	Asp	Arg	Glu										
145					150										

<210> 156  
<211> 81  
<212> PRT  
<213> Homo sapiens

<400> 156

Leu	Pro	Val	Ala	Ala	Gly	Gly	Arg	Gly	Gln	Asp	Ala	Gln	Leu	Arg	Pro
1				5					10					15	
Glu	Leu	Ser	Gly	Val	Val	Ser	Arg	Pro	Arg	Leu	Gly	Gly	Gly	Ala	Pro
			20					25					30		
Ser	Arg	Ser	Arg	Gly	Arg	Arg	Ile	Gly	Trp	Ala	Arg	Val	Ser	Ser	Pro
		35					40					45			
Ala	Gly	Arg	Arg	Asp	Arg	Val	Cys	Gly	Gly	Gly	Leu	Gly	Ala	Ser	Ala
	50					55					60				

Gly	Arg	Ala	His	Ala	Gly	Gly	Ala	Ala	Arg	Gly	Ala	Gly	Pro	Leu	Arg
65					70					75					80

Gly

&lt;210&gt; 157

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 157

Pro	Gly	Ser	Gln	Ser	Val	Thr	Pro	Pro	Met	Ala	Glu	Pro	Leu	Gln	Pro
1				5					10					15	
Asp	Pro	Gly	Ala	Ala	Glu	Asp	Ala	Ala	Ala	Gln	Ala	Val	Glu	Thr	Pro
			20					25					30		
Gly	Trp	Lys	Ala	Pro	Glu	Asp	Ala	Gly	Pro	Gln	Pro	Gly	Ser	Tyr	Glu
		35					40					45			
Ile	Arg	His	Tyr	Gly	Pro	Ala	Lys	Trp	Val	Ser	Thr	Ser	Val	Glu	Ser
	50					55					60				
Met	Asp	Trp	Asp	Ser	Ala	Ile	Gln	Thr	Gly	Phe	Thr	Lys	Leu	Asn	Ser
65					70					75					80
Tyr	Ile	Gln	Gly	Lys	Asn	Glu	Lys	Glu	Met	Lys	Ile	Lys	Met	Thr	Ala
				85					90					95	
Pro	Val	Thr	Ser	Tyr	Val	Glu	Pro	Gly	Ser	Gly	Pro	Phe	Ser	Glu	Ser
			100					105					110		
Thr	Ile	Thr	Ile	Ser	Leu	Tyr	Ile	Pro	Ser	Glu	Gln	Gln	Phe	Asp	Pro
		115					120					125			
Pro	Arg	Pro	Leu	Glu	Ser	Asp	Val	Phe	Ile	Glu	Asp	Arg	Ala	Glu	Met
	130					135					140				
Thr	Val	Phe	Val	Arg	Ser	Phe	Asp	Gly	Phe	Ser	Ser	Ala	Gln	Lys	Asn
145					150					155					160
Gln	Glu	Gln	Leu	Leu	Thr	Leu	Ala	Ser	Ile	Leu	Arg	Glu	Asp	Gly	Lys
				165					170					175	
Val	Phe	Asp	Glu	Lys	Val	Tyr	Tyr	Thr	Ala	Gly	Tyr	Asn	Ser	Pro	Val
			180					185					190		
Lys	Leu	Leu	Asn	Arg	Asn	Asn	Glu	Val	Trp	Leu	Ile	Gln	Lys	Asn	Glu
		195					200					205			
Pro	Thr	Lys	Glu	Asn	Glu										
	210														

&lt;210&gt; 158

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

Pro	Asn	Phe	Tyr	Arg	Gly	Phe	Ile	Phe	Asn	Leu	Thr	Met	Cys	Gly	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1				5					10					15		
Leu	Ser	Cys	Leu 20	Asn	Leu	Phe	Arg	Ala 25	Val	Cys	Ser	Val	His 30	Gln	Met	
Gly	Arg	Ser 35	Gly	Met	Gly	His	Leu 40	Arg	Pro	Phe	Arg	Ser 45	Gly	Leu	Asn	
Arg	Met 50	Leu	Glu	Pro	Arg	Leu 55	Asp	Ser	Asp	Thr	Leu 60	Arg	Phe			

<210> 159  
 <211> 104  
 <212> PRT  
 <213> Homo sapiens

<400> 159

Ile 1	His	Leu	Pro	Lys 5	Lys	Leu	Ile	Ser	Phe 10	Tyr	Leu	Arg	Gly	Glu 15	Val	
Gln	Phe	Ser	Phe 20	Gly	Ser	Ser	Glu	Ser 25	Lys	His	Leu	Ile	Cys 30	Trp	Val	
Trp	Lys	Thr 35	Pro	Phe	Leu	Ala	Phe 40	Tyr	Val	Leu	Ser	His 45	Asn	Asn	Ser	
Ile	Lys 50	Gln	Glu	Gly	Lys	Gln 55	Lys	Thr	Lys	Lys	Lys 60	Lys	Gly	Lys	Lys	
Lys 65	Asn	Leu	His	Gly	Leu 70	Val	Ser	Leu	Thr	Lys 75	His	Val	Gly	Ala	Val 80	
Cys	Leu	Gly	Gly	Ala 85	Gly	Tyr	Arg	Thr	Cys 90	Gln	Cys	Leu	Gly	Phe 95	Ser	
Ile	Asn	Leu	Ala 100	Arg	Asp	Ile	Lys									

<210> 160  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<400> 160

Ser 1	Leu	Leu	Ile	Ser 5	Arg	Lys	Ile	Lys	Gln 10	Asn	Thr	Ser	Pro	Ala 15	Arg	
Leu	Thr	Cys	Val 20	Tyr	Ile	Tyr	Ile	Lys 25	Gln	Arg	Ala	Thr	Pro 30	Thr	Ser	
Gln	Gln	Leu 35	Gly	Glu	Ile	Ser	Ala 40	Val	His	Ala	Val	Val 45	Cys	Gln	Phe	
Gly	Glu 50	Ile	Thr	Pro	Trp	Lys 55	Asn	Trp	Lys	Asn	Leu 60	Leu	Ala	Gly	Lys	
Asn 65	Ser	Phe	Ile	Cys	Ile 70	Lys	Ser	Val	Leu	Gln 75	Lys	Asn	Pro	Cys	Gly 80	

<210> 161  
 <400> 161

000

&lt;210&gt; 162

&lt;400&gt; 162

000

&lt;210&gt; 163

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 163

Pro	Ser	Ile	Asp	Leu	Glu	Ala	Glu	Glu	Ser	Gln	Arg	Leu	Leu	Lys	Val
1				5					10					15	
Val	Met	Trp	Phe	Ser	Phe	Lys	Lys	Leu	Leu	Phe	Leu	Glu	Ser	Arg	Ile
			20					25					30		
Tyr	Gly	Tyr	Asn	Val	Cys	Ser	Leu	Phe	Val	His	Lys	Ile	Lys	Pro	Phe
		35					40					45			
Lys	Lys	Leu	Lys	Lys	Lys	Lys	Lys	Arg	Gly	Glu	Lys	Lys	Arg	Glu	Lys
	50					55					60				
Gly	Lys	Gly	Lys	Arg	Lys	Arg	Arg	Gly	Glu	Glu					
65					70					75					

&lt;210&gt; 164

&lt;211&gt; 68

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

Lys	Tyr	Leu	Thr	Leu	Pro	Tyr	Lys	Leu	Leu	Val	Pro	Phe	Cys	Ile	Pro
1				5					10					15	
Pro	Ser	Ile	Thr	Leu	Thr	Lys	Gly	Ile	Phe	Tyr	Cys	Lys	Glu	Tyr	Phe
			20					25					30		
Ile	Leu	Tyr	Ile	Thr	Ser	His	Glu	Phe	Leu	Pro	Leu	Val	Thr	Ile	Gln
		35					40					45			
Met	Leu	Pro	Ser	Ala	Ile	Ile	Gln	Ile	Ala	Gln	Pro	Phe	Tyr	Val	His
	50					55					60				
Asn	Ser	Leu	Leu												
65															

&lt;210&gt; 165

&lt;211&gt; 66

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

Leu	Phe	Phe	Leu	Phe	Arg	Tyr	His	Thr	Val	Pro	Leu	Pro	Pro	Lys	Gly
1				5					10					15	
Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys	Gln	Thr	Gln	Met	Lys	Leu
			20					25					30		

Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met	Phe	Gly	Ile	Leu	Asn	Gly
		35					40					45			
Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr	Leu	Glu	Lys	Thr	Ile	His
	50					55					60				
Glu	Glu														
65															

<210> 166  
 <211> 159  
 <212> PRT  
 <213> Homo sapiens

<400> 166

Thr	Arg	Leu	Lys	Gly	Asp	Arg	Gly	Gly	Val	His	Phe	Leu	Lys	Ala	Leu
1				5					10					15	
Arg	Arg	Gly	Gly	Leu	Arg	Ala	Ser	Leu	Leu	Tyr	Leu	Leu	Glu	Lys	Tyr
			20					25					30		
Arg	Leu	Val	Phe	Leu	Leu	Ser	Ile	Cys	Val	Arg	Gly	Met	Val	Ser	Ser
		35					40					45			
Val	Lys	Ser	Phe	Leu	Val	Gly	Glu	Gln	Leu	Leu	Ser	Ile	Ser	Glu	Pro
	50					55					60				
Arg	Phe	Lys	Met	Ser	Val	Cys	Lys	Cys	Ser	Phe	Leu	Ser	Thr	Thr	Ser
65					70					75					80
Thr	Phe	Val	Pro	Ile	Ser	Ser	Asp	Ser	Lys	Lys	Val	Ser	Ser	Tyr	Phe
				85					90					95	
Ser	Leu	Cys	Ser	Glu	Ser	Leu	Ala	Glu	Gln	Asn	Leu	Phe	Met	Met	Pro
			100					105					110		
Glu	Val	Phe	Cys	Ser	Glu	Gln	Lys	Phe	Asp	Pro	Glu	Leu	Asn	Asp	Leu
		115					120					125			
Ser	Phe	Phe	Phe	Thr	Arg	Leu	Phe	Ser	Ser	Leu	Val	Thr	Leu	Arg	Val
	130					135					140				
Ser	Pro	His	Ala	Pro	Ala	Ser	Glu	Met	Gln	Thr	Val	Leu	Ser	Ser	
145					150					155					

<210> 167  
 <211> 439  
 <212> PRT  
 <213> Homo sapiens

<400> 167

Lys	Ser	Leu	Leu	Phe	Thr	Ser	Ser	Lys	Phe	Pro	Leu	Ile	Ser	Phe	Ser
1				5					10					15	
Ser	Pro	Gln	Gly	Leu	Lys	Phe	Arg	Ser	Lys	Ser	Ser	Leu	Ala	Asn	Tyr
			20					25					30		
Leu	His	Lys	Asn	Gly	Glu	Thr	Ser	Leu	Lys	Pro	Glu	Asp	Phe	Asp	Phe
		35					40					45			
Thr	Val	Leu	Ser	Lys	Arg	Gly	Ile	Lys	Ser	Arg	Tyr	Lys	Asp	Cys	Ser



	50					55					60				
Met 65	Ala	Ala	Leu	Thr	Ser 70	His	Leu	Gln	Asn	Gln 75	Ser	Asn	Asn	Ser	Asn 80
Trp	Asn	Leu	Arg	Thr 85	Arg	Ser	Lys	Cys	Lys 90	Lys	Asp	Val	Phe	Met 95	Pro
Pro	Ser	Ser	Ser 100	Ser	Glu	Leu	Gln	Glu 105	Ser	Arg	Gly	Leu	Ser 110	Asn	Phe
Thr	Ser	Thr 115	His	Leu	Leu	Leu	Lys 120	Glu	Asp	Glu	Gly	Val 125	Asp	Asp	Val
Asn	Phe 130	Arg	Lys	Val	Arg	Lys 135	Pro	Lys	Gly	Lys	Val 140	Thr	Ile	Leu	Lys
Gly 145	Ile	Pro	Ile	Lys	Lys 150	Thr	Lys	Lys	Gly	Cys 155	Arg	Lys	Ser	Cys	Ser 160
Gly	Phe	Val	Gln	Ser 165	Asp	Ser	Lys	Arg	Glu 170	Ser	Val	Cys	Asn	Lys 175	Ala
Asp	Ala	Glu	Ser 180	Glu	Pro	Val	Ala	Gln 185	Lys	Ser	Gln	Leu	Asp 190	Arg	Thr
Val	Cys	Ile 195	Ser	Asp	Ala	Gly	Ala 200	Cys	Gly	Glu	Thr	Leu 205	Ser	Val	Thr
Ser	Glu 210	Glu	Asn	Ser	Leu	Val 215	Lys	Lys	Lys	Glu	Arg 220	Ser	Leu	Ser	Ser
Gly 225	Ser	Asn	Phe	Cys	Ser 230	Glu	Gln	Lys	Thr	Ser 235	Gly	Ile	Ile	Asn	Lys 240
Phe	Cys	Ser	Ala	Lys 245	Asp	Ser	Glu	His	Asn 250	Glu	Lys	Tyr	Glu	Asp 255	Thr
Phe	Leu	Glu	Ser 260	Glu	Glu	Ile	Gly	Thr 265	Lys	Val	Glu	Val	Val 270	Glu	Arg
Lys	Glu	His 275	Leu	His	Thr	Asp	Ile 280	Leu	Lys	Arg	Gly	Ser 285	Glu	Met	Asp
Asn	Asn 290	Cys	Ser	Pro	Thr	Arg 295	Lys	Asp	Phe	Thr	Glu 300	Asp	Thr	Ile	Pro
Arg 305	Thr	Gln	Ile	Glu	Arg 310	Arg	Lys	Thr	Ser	Leu 315	Tyr	Phe	Ser	Ser	Lys 320
Tyr	Asn	Lys	Glu	Ala 325	Leu	Ser	Pro	Pro	Arg 330	Arg	Lys	Ala	Phe	Lys 335	Lys
Trp	Thr	Pro	Pro 340	Arg	Ser	Pro	Phe	Asn 345	Leu	Val	Gln	Glu	Thr 350	Leu	Phe
His	Asp	Pro 355	Trp	Lys	Leu	Leu	Ile 360	Ala	Thr	Ile	Phe	Leu 365	Asn	Arg	Thr
Ser	Gly 370	Lys	Met	Ala	Ile	Pro 375	Val	Leu	Trp	Lys	Phe 380	Leu	Glu	Lys	Tyr
Pro	Ser	Ala	Glu	Val	Ala	Arg	Thr	Ala	Asp	Trp	Arg	Asp	Val	Ser	Glu

385					390					395					400
Leu	Leu	Lys	Pro	Leu 405	Gly	Leu	Tyr	Asp	Leu 410	Arg	Ala	Lys	Thr	Ile 415	Val
Lys	Phe	Ser	Asp 420	Glu	Tyr	Leu	Thr	Lys 425	Gln	Trp	Lys	Tyr	Pro 430	Ile	Glu
Leu	His	Gly 435	Ile	Gly	Ala	Pro									

<210> 168  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 168

Asp 1	Cys	Gly	Lys	Val 5	Gln	Thr	Gln	Met	Gln 10	Phe	Ala	Leu	Thr	Asn 15	Phe
Leu	Gly	Leu	Ile 20	Ser	Leu	Cys	Lys	Thr 25	Pro	Val	Leu	Ser	Phe 30	Leu	Pro
Gln	Asp	Arg 35	Val	Gln	Ser	Phe	Leu 40	Lys	His	Ala	Leu	Arg 45	Cys	Pro	His
Leu	Arg 50	His	Cys	Phe	Val	Asp 55	Thr	Leu	Lys	Gly	Val 60	His	Lys	Ala	Lys
Lys 65	Ser	Asp	Gln	Met	Leu 70	Arg	Ala	Ser	Asn	Leu 75	Tyr	Leu	Thr	Thr	Trp 80
Thr	Trp	His	Trp	Gln 85	Lys	Ser	Leu	Gln	His 90						

<210> 169  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 169

Ser 1	Asp	Phe	Cys	Gln 5	Cys	His	Val	Gln	Val 10	Val	Arg	Tyr	Lys	Leu 15	Leu
Ala	Leu	Ser	Ile 20	Trp	Ser	Asp	Phe	Phe 25	Ala	Leu	Trp	Thr	Pro 30	Leu	Arg
Val	Ser	Thr 35	Lys	Gln	Cys	Leu	Arg 40	Cys	Gly	His	Leu	Arg 45	Ala	Cys	Phe
Arg	Lys 50	Leu	Cys	Thr	Leu	Ser 55	Cys	Gly	Arg	Lys	Glu 60	Arg	Thr	Gly	Val
Leu 65	His	Lys	Glu	Ile	Ser 70	Pro	Arg	Lys	Leu	Val 75	Asn	Ala	Asn	Cys	Ile 80
Cys	Val	Cys	Thr	Leu 85	Pro	Gln	Ser	Tyr	Ile 90	Val	Phe				

<210> 170  
 <211> 91

<212> PRT  
 <213> Homo sapiens

<400> 170

Ala 1	Asp	Ser	His	Gln 5	Asn	Tyr	Ile	Pro	Trp 10	Pro	Pro	Ala	Cys	Val 15	Leu	
Leu	Ala	Arg	Pro 20	Trp	Leu	Ala	Ser	Leu 25	Thr	Arg	Glu	Lys	Asp 30	Leu	Gln	
Lys	Ile	Arg 35	Leu	Trp	Asp	His	Phe 40	Val	Cys	Ala	Leu	Gly 45	Met	Thr	Phe	
Phe	Pro 50	Thr	Pro	Gly	Lys	Pro 55	Leu	Gly	Leu	Ser	Glu 60	Thr	Leu	Trp	Leu	
Ala 65	Asn	His	Met	Val	Ser 70	Leu	Lys	Val	Glu	Arg 75	Leu	Ser	Asn	Pro	Pro 80	
Ile	Pro	Arg	Glu	Phe 85	Gln	Ser	Val	Asp	Val 90	Ile						

<210> 171  
 <211> 95  
 <212> PRT  
 <213> Homo sapiens

<400> 171

Asn 1	Gly	Gly	Leu	Asn 5	Ala	His	Leu	Ala	Ser 10	Ala	Ser	Glu	Phe	Asp 15	His	
Ser	Gly	Val	Gln 20	Leu	Ile	Glu	Arg	Glu 25	Glu	Glu	Ile	Cys	Ile 30	Phe	Tyr	
Glu	Lys	Ile 35	Asn	Ile	Gln	Glu	Lys 40	Met	Lys	Leu	Asn	Gly 45	Glu	Ile	Glu	
Ile	His 50	Leu	Leu	Glu	Glu	Lys 55	Ile	Gln	Phe	Leu	Lys 60	Met	Lys	Ile	Ala	
Glu 65	Lys	Gln	Arg	Gln	Ile 70	Cys	Val	Thr	Gln	Lys 75	Leu	Leu	Pro	Ala	Lys 80	
Arg	Ser	Leu	Asp	Ala 85	Asp	Leu	Ala	Val	Leu 90	Gln	Ile	Gln	Phe	Ser 95		

<210> 172  
 <211> 90  
 <212> PRT  
 <213> Homo sapiens

<400> 172

Lys 1	Thr	Glu	Phe	Gly 5	Ala	Gln	Leu	Gly	Arg 10	His	Pro	Gly	Thr	Ser 15	Trp	
Leu	Ala	Val	Ile 20	Ser	Gly	Ser	His	Lys 25	Phe	Val	Phe	Ala	Ser 30	Gln	Gln	
Ser	Ser	Phe 35	Ser	Gly	Ile	Gly	Ser 40	Phe	Leu	Pro	Val	Asp 45	Val	Phe	Gln	

Phe	Leu	His	Leu	Val	Ser	Ser	Ser	Leu	Gly	Tyr	Leu	Phe	Phe	His	Lys
	50					55					60				
Lys	Cys	Ile	Phe	Leu	Leu	Pro	Ala	Leu	Ser	Ala	Glu	Arg	His	Tyr	Gly
65					70					75					80
Gln	Ile	Gln	Arg	Gln	Arg	Leu	Ser	Gly	His						
				85					90						

&lt;210&gt; 173

&lt;211&gt; 102

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 173

Ala	Val	Arg	Ser	Arg	Gly	Ala	Leu	Ser	Leu	Ser	Val	Gly	Ala	Ala	Cys
1				5					10					15	
Gly	Leu	Val	Ala	Leu	Trp	Gln	Arg	Arg	Arg	Gln	Asp	Ser	Gly	Thr	Met
			20					25					30		
Ser	Gly	Phe	Ser	Thr	Glu	Glu	Arg	Ala	Ala	Pro	Phe	Ser	Leu	Glu	Tyr
		35					40					45			
Arg	Val	Phe	Leu	Lys	Asn	Glu	Lys	Gly	Gln	Tyr	Ile	Ser	Pro	Phe	His
	50					55					60				
Asp	Ile	Pro	Ile	Tyr	Ala	Asp	Lys	Val	Arg	His	Pro	Cys	Phe	Trp	Thr
65					70					75					80
Gln	Ser	Leu	Tyr	Ser	Asp	Gln	Leu	Val	Leu	His	Met	Asn	Phe	Leu	Ile
				85					90					95	
Cys	Leu	Ser	Thr	Ser	Ala										
			100												

&lt;210&gt; 174

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 174

Val	Lys	Arg	Leu	Cys	Pro	Lys	Thr	Arg	Met	Pro	Tyr	Leu	Ile	Cys	Ile
1				5					10					15	
Asn	Trp	Asn	Ile	Met	Lys	Trp	Arg	Tyr	Ile	Leu	Ser	Phe	Leu	Ile	Phe
			20					25					30		
Glu	Glu	Asp	Ser	Val	Leu	Gln	Gly	Glu	Gly	Arg	Gly	Ala	Leu	Leu	Gly
		35					40					45			
Ala	Glu	Ala	Ala	His	Ser	Ala	Gly	Val	Leu	Pro	Pro	Pro	Leu	Pro	Gln
	50					55					60				
Ser	His	Gln	Pro	Ala	Arg	Gly	Ala	Asp							
65					70										

&lt;210&gt; 175

&lt;211&gt; 130

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 175

Arg	Arg	Gln	Arg	Lys	Ala	Glu	Pro	Gly	Ala	Cys	Ala	Leu	Gly	Arg	Val
1				5					10					15	
Gly	Ser	Glu	Cys	Ile	Pro	Glu	Pro	Gly	Ala	Arg	Arg	Thr	Ala	Gln	Ala
			20					25					30		
Ala	Gly	Leu	Arg	Ser	Val	Ser	Gly	Ala	Ala	Asn	Thr	Lys	Val	Arg	Glu
		35					40					45			
Leu	Lys	His	Phe	Arg	Phe	Leu	Gly	Leu	Leu	Arg	Ser	Cys	Arg	Ser	Glu
	50					55					60				
Met	Glu	Val	Asp	Ala	Pro	Gly	Val	Asp	Gly	Arg	Asp	Gly	Leu	Arg	Glu
65					70					75					80
Arg	Arg	Gly	Phe	Ser	Glu	Gly	Gly	Arg	Gln	Asn	Phe	Asp	Val	Arg	Pro
				85					90					95	
Gln	Ser	Gly	Ala	Asn	Gly	Leu	Pro	Lys	His	Ser	Tyr	Trp	Leu	Asp	Leu
			100					105					110		
Trp	Leu	Phe	Ile	Leu	Phe	Asp	Val	Val	Val	Phe	Leu	Phe	Val	Tyr	Phe
		115					120					125			
Leu	Pro														
	130														

&lt;210&gt; 176

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 176

Ile	Leu	Lys	Met	Ala	Thr	Asn	Phe	Leu	Asn	Lys	Glu	Asp	Arg	Thr	Leu
1				5					10					15	
Asn	Arg	Arg	Ile	Ser	His	Leu	Gln	Gly	Thr	Leu	Pro	Phe	Ile	Leu	His
			20					25					30		
Phe	Val	Thr	Asn	Leu	Gln	Asn	Ser	Ile	Asn	Trp	Val	Gly	Phe	His	Pro
		35					40					45			
Phe	Leu	Ala	Lys	Phe	Leu	Lys	Leu	Asn	Pro	Leu	Val	Arg	Val		
	50					55					60				

&lt;210&gt; 177

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 177

Ala	Val	Tyr	Cys	Ile	Leu	His	Gln	Gln	Lys	Val	Leu	Arg	Leu	Tyr	Lys
1				5					10					15	
Arg	Ala	Leu	Arg	His	Leu	Glu	Ser	Trp	Cys	Val	Gln	Arg	Asp	Lys	Tyr
			20					25					30		

Arg	Tyr	Phe 35	Ala	Cys	Leu	Met	Arg 40	Ala	Arg	Phe	Glu	Glu 45	His	Lys	Asn
Glu	Lys 50	Asp	Met	Ala	Lys	Ala 55	Thr	Gln	Leu	Leu	Lys 60	Glu	Ala	Glu	Glu
Glu 65	Phe	Trp	Tyr	Arg	Gln 70	His	Pro	Gln	Pro	Tyr 75	Ile	Phe	Pro	Asp	Ser 80
Pro	Gly	Gly	Thr	Ser 85	Tyr	Glu	Arg	Tyr	Asp 90	Cys	Tyr	Lys	Val	Pro 95	Glu
Trp	Cys	Leu	Asp 100	Asp	Trp	His	Pro	Ser 105	Glu	Lys	Ala	Met	Tyr 110	Pro	Asp
Tyr	Phe	Ala 115	Lys	Arg	Glu	Gln	Trp 120	Lys	Lys	Leu	Arg	Arg 125	Glu	Ser	Trp
Glu	Arg 130	Glu	Val	Lys	Gln	Leu 135	Gln	Glu	Glu	Thr	Pro 140	Pro	Gly	Gly	Pro
Leu 145	Thr	Glu	Ala	Leu	Pro 150	Pro	Ala	Arg	Lys	Glu 155	Gly	Asp	Leu	Pro	Pro 160
Leu	Trp	Trp	Tyr	Ile 165	Val	Thr	Arg	Pro	Arg 170	Glu	Arg	Pro	Met		

&lt;210&gt; 178

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

Pro 1	Leu	Val	Pro	Ser 5	Phe	Pro	Ser	Ala	Val 10	Ser	Ser	Thr	Val	Leu 15	Ser
Trp	Gln	Ser	Asn 20	Gln	Asp	Thr	Leu	Pro 25	Ser	Gln	Lys	Asp	Ala 30	Ser	His
Leu	Ser	Thr 35	Ile	Leu	Gly	Pro	Cys 40	Ser	Asn	Arg	Ile	Ser 45	His	Arg	Arg
Cys	Pro 50	Gln	Glu	Ser	Gln	Gly 55	Arg	Cys	Met	Ala	Val 60	Asp	Ala	Asp	Gly
Thr 65	Arg	Ile	Leu	Pro	Arg 70	Pro	Pro	Ser	Ala	Ala 75	Gly	Trp	Pro	Ser	Pro 80
Tyr	Pro	Phe	His	Ser 85	Tyr	Val	Leu	Gln	Thr 90	Gly	Leu	Ser	Ser	Asn 95	Lys
Gln	Ser	Ile	Gly 100	Ile	Cys	Leu	Ser	Gly 105	Arg	Thr	Thr	Thr	Arg 110	Gly	Gly
Val	Ala	Pro 115	Ala	Tyr	Lys	Ala	Ala 120	Thr	Pro	Phe	Ala	Asp 125	Val	Val	Cys
Asn	Ile 130	Arg													

&lt;210&gt; 179

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 179

Leu 1	Met	Met	Thr	Ile 5	Tyr	Ala	Leu	Ser	Asn 10	Glu	Phe	Ala	Phe	Lys 15	Ile
Asn	Glu	Glu	Gln 20	Leu	Ser	Phe	Phe	Pro 25	Leu	Leu	Ser	Val	Gln 30	Leu	Trp
His	Ala	Gln 35	Arg	Phe	Leu	Leu	Asp 40	Ser	Ser	Trp	Ser	Gly 45	Val	Ile	Pro
Phe	Phe 50	Phe	Ser	Cys	Ser	Cys 55	Leu	Pro	Phe	Leu	Tyr 60	Pro	Pro	Lys	Trp
Arg 65	Gln	Ile	His	Asp	Leu 70	Lys	Asp	Thr	Gln	Tyr 75	Leu	Leu	Asn	Ser	Ser 80

&lt;210&gt; 180

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

Lys 1	Val	Leu	Arg	Lys 5	Leu	Lys	Gly	Pro	Glu 10	Glu	Ala	Ser	Gly	Gln 15	Met
Ala	Gly	Ala	Gly 20	Pro	Thr	Met	Leu	Leu 25	Arg	Glu	Glu	Asn	Gly 30	Cys	Cys
Ser	Arg	Arg 35	Gln	Ser	Ser	Ser	Ser 40	Ala	Gly	Asp	Ser	Asp 45	Gly	Glu	Arg
Glu	Asp 50	Ser	Ala	Ala	Glu	Arg 55	Ala	Arg	Gln	Gln	Leu 60	Glu	Ala	Leu	Leu
Asn 65	Lys	Thr	Met	Arg	Ile 70	Arg	Met	Thr	Asp	Gly 75	Arg	Thr	Leu	Val	Gly 80
Cys	Phe	Leu	Cys	Thr 85	Asp	Arg	Asp	Cys	Asn 90	Val	Ile	Leu	Gly	Ser 95	Ala
Gln	Glu	Phe	Leu 100	Lys	Pro	Ser	Asp	Ser 105	Phe	Ser	Ala	Gly	Glu 110	Pro	Arg
Val	Leu	Gly 115	Leu	Ala	Met	Val	Pro 120	Gly	His	His	Ile	Val 125	Ser	Ile	Glu
Val	Gln 130	Arg	Glu	Ser	Leu	Thr 135	Gly	Pro	Pro	Tyr	Leu 140				

&lt;210&gt; 181

&lt;211&gt; 114

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 181

Ser 1	Leu	Lys	Gly	Lys 5	Arg	His	Arg	Gly	Gln 10	Arg	Tyr	Gly	Gly	Pro 15	Val
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Arg	Leu	Ser	Leu 20	Cys	Thr	Ser	Met	Glu 25	Thr	Met	Trp	Cys	Pro 30	Gly	Thr
Met	Ala	Arg 35	Pro	Ser	Thr	Arg	Gly 40	Ser	Pro	Ala	Glu	Lys 45	Glu	Ser	Asp
Gly	Leu 50	Arg	Asn	Ser	Cys	Ala 55	Glu	Pro	Arg	Met	Thr 60	Leu	Gln	Ser	Arg
Ser 65	Val	Gln	Arg	Lys	Gln 70	Pro	Thr	Ser	Val	Arg 75	Pro	Ser	Val	Met	Arg 80
Met	Arg	Ile	Val	Leu 85	Leu	Ser	Ser	Ala	Ser 90	Ser	Cys	Cys	Arg	Ala 95	Arg
Ser	Ala	Ala	Glu 100	Ser	Ser	Arg	Ser	Pro 105	Ser	Glu	Ser	Pro	Ala 110	Leu	Glu

Leu Leu

<210> 182

<211> 95

<212> PRT

<213> Homo sapiens

<400> 182

Arg 1	Leu	Ser	Arg	Leu 5	Thr	Glu	Pro	Lys	Glu 10	Asp	Pro	Met	Ala	Gly 15	Ile
Ser	Thr	Ala	Glu 20	His	His	Leu	Asp	Pro 25	Thr	Ala	Ala	Leu	Pro 30	Thr	Gln
Leu	Ser	Arg 35	Ser	Arg	His	Ser	Pro 40	Gln	Val	Ile	Ser	Thr 45	Asp	Gly	Gly
Glu 50	Thr	Arg	Gly	Cys	Gly	Arg 55	Gln	Glu	Arg	Lys	Ala 60	Glu	Arg	Arg	Val
Cys 65	Lys	Asn	Ala	Lys	Val 70	Thr	Phe	Pro	Ile	Val 75	Gly	Gly	Lys	Cys	Gln 80
Arg	His	Trp	Phe	Cys 85	Cys	His	Arg	Gln	Ser 90	Glu	His	Leu	Glu	Leu 95	

<210> 183

<211> 131

<212> PRT

<213> Homo sapiens

<400> 183

Arg 1	Arg	Val	Gln	His 5	Pro	Pro	Phe	Phe	Ser 10	Gln	Leu	Ile	Arg	Asp 15	Ala
Ala	Lys	Arg	Thr 20	Phe	Arg	Ile	Thr	Arg 25	Leu	Gln	Ala	Phe	Ser 30	Lys	Tyr
Leu	Val	Val 35	Tyr	Val	Tyr	Leu	Asn 40	Gly	Ser	Met	Leu	Pro 45	Val	Pro	Ser
Pro	Cys	Pro	Leu	Cys	Gln	Pro	Pro	Val	Ala	Leu	Val	Leu	Val	Ser	Phe



50					55					60					
Pro 65	Ser	Ser	Ala	Lys	Arg 70	Pro	Trp	Asn	Leu	Asn 75	Gly	Gly	Cys	Phe	Ala 80
Leu	Gly	Gly	Ser	Cys 85	Trp	Trp	Asp	Gln	Ser 90	Phe	Asp	Lys	Pro	Pro 95	Ala
Pro	Trp	Trp	His 100	Leu	Ser	Trp	Lys	Asp 105	Val	Thr	Thr	Pro	Gly 110	Ala	Gln
Thr	Ala	Cys 115	Gly	Ser	Arg	Thr	Ser 120	Ala	Phe	Gly	Ile	Phe 125	Leu	Pro	Gln
Trp	Gly 130	Arg													

&lt;210&gt; 184

&lt;211&gt; 128

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

Thr 1	Ala	Pro	Cys	Cys 5	Arg	Cys	Pro	Ala	Pro 10	Val	Pro	Ser	Val	Asn 15	Pro
Leu	Ser	Leu	Trp 20	Cys	Trp	Phe	Arg	Ser 25	Arg	Leu	Gln	Gln	Asn 30	Asp	Leu
Gly	Thr	Ser 35	Met	Gly	Ala	Ala	Leu 40	Leu	Trp	Glu	Val	Leu 45	Val	Gly	Gly
Thr	Arg 50	Ala	Leu	Thr	Asn	Leu 55	Leu	Leu	Leu	Gly	Gly 60	Thr	Ser	Pro	Gly
Arg 65	Thr	Ser	Gln	Leu	Gln 70	Val	Leu	Arg	Leu	Pro 75	Val	Ala	Ala	Glu	Pro 80
Val	Pro	Leu	Ala	Phe 85	Ser	Ser	His	Asn	Gly 90	Glu	Gly	Asp	Phe	Gly 95	Ile
Leu	Thr	Asn 100	Ser	Ser	Leu	Gly	Leu	Ser 105	Leu	Leu	Pro	Ser	Thr 110	Ala	Ser
Arg	Phe	Ser 115	Ser	Ile	Cys	Ala	Tyr 120	Tyr	Leu	Arg	Thr	Val 125	Ser	Ala	Pro

&lt;210&gt; 185

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

Asp 1	Ser	Arg	Val	Tyr 5	Cys	Phe	Ser	Gly	Asn 10	Tyr	Arg	Lys	Leu	Val 15	Leu
Pro	Arg	Lys	Thr 20	Gly	Ala	Ile	Arg	Asn 25	Gly	Ser	Asn	Ile	Ser 30	Lys	Leu
Arg	Lys	Gln 35	Asp	Val	Leu	Ser	Phe 40	Ala	His	Leu	Gly	Phe 45	Leu	Leu	Phe

Pro Phe Ser Leu Phe Ser Leu Arg Ser Leu Phe Gln Phe Pro Ser Asp  
 50 55 60  
 Leu Pro Leu Val Pro Leu Glu Ser Gln Arg Leu  
 65 70 75  
 <210> 186  
 <211> 62  
 <212> PRT  
 <213> Homo sapiens

<400> 186  
 Leu Gly Asp Ser Glu Ser Met Pro Leu Leu Ala Leu Lys Cys Pro Val  
 1 5 10 15  
 Arg Leu Leu Gly Thr Leu Glu Pro Ser Glu Ile Leu Ile Ile Leu Gly  
 20 25 30  
 Ser Ser Pro Tyr Phe Gln Met Phe Ser Ala Gln His Trp Val Leu Ser  
 35 40 45  
 Ser Thr Thr Glu Asn Pro Glu Glu Lys Gly Arg Cys Phe Pro  
 50 55 60  
 <210> 187  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 187  
 Pro His Pro Ser Arg Arg Leu Thr Gln Gly Arg Trp Val Arg Lys Ser  
 1 5 10 15  
 Arg Val Ala Met Glu Lys Ile Pro Val Ser Ala Phe Leu Arg Leu Val  
 20 25 30  
 Ala Leu Ser Tyr Asn Leu Ala Arg Asp Ser Thr Val Lys Pro Gly Ala  
 35 40 45  
 Lys Lys Asp Arg Lys Glu Ser Arg Ala Lys Leu Arg Gln Thr Leu Ser  
 50 55 60  
 Arg Ser Trp Gly Glu Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala  
 65 70 75 80  
 Leu Tyr Lys Ser Arg Leu Ala Thr Asn  
 85

<210> 188  
 <211> 72  
 <212> PRT  
 <213> Homo sapiens

<400> 188  
 Gly Asn Pro Glu Leu Pro Trp Arg Lys Phe Gln Cys Gln His Ser Cys  
 1 5 10 15  
 Ala Leu Trp Arg Ser Pro Thr Ile Trp Pro Gly Ile Ala Gln Ser Asn  
 20 25 30

Leu	Glu	Pro 35	Lys	Arg	Thr	Gly	Arg 40	Ser	Leu	Glu	Pro	Asn 45	Cys	Ala	Arg
Pro	Ser 50	Pro	Glu	Val	Gly	Val 55	Asn	Asn	Ser	Ser	Gly 60	Leu	Arg	Arg	Met
Lys 65	Lys	Leu	Tyr	Ile	Asn 70	Arg	Asp								

&lt;210&gt; 189

&lt;211&gt; 125

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 189

Ser 1	Leu	Gly	His	Arg 5	Pro	Arg	Asn	Gly	Gly 10	His	Ser	Arg	Gly	Cys 15	Asp
Leu	Gly	Gly	Leu 20	His	Ala	His	Ser	Pro 25	Asp	Pro	Arg	Leu	Gln 30	Gly	Ala
Gly	Leu	Gln 35	Gln	Ala	Lys	Asn	Ala 40	Ala	Tyr	Ser	Val	Ser 45	Leu	Pro	Pro
Gly	Cys 50	Val	Gly	His	Leu	Trp 55	Pro	His	Leu	Arg	Leu 60	His	His	Arg	Thr
Gly 65	Arg	Glu	His	Arg	Ala 70	His	Thr	Leu	Leu	Pro 75	Leu	Trp	Asp	Pro	Leu 80
Phe	His	Leu	Leu	Leu 85	Leu	Pro	Ala	Gly	Ser 90	Cys	Cys	Gln	Ser	Asp 95	Gln
Ala	Arg	Pro	Gly 100	Glu	Glu	Ala	Pro	Phe 105	Pro	Val	Gly	Asp	Ser 110	Gly	Ser
Gly	Arg	Gly 115	Leu	Gln	Pro	Ser	Pro 120	Gly	Cys	Tyr	Arg	Tyr 125			

&lt;210&gt; 190

&lt;211&gt; 200

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

Arg 1	Gly	Arg	Asp	Ser 5	Cys	Pro	Arg	Ser	Pro 10	Pro	Ala	Leu	Arg	Ser 15	Ser
Pro	Ala	Ala	Leu 20	Leu	Arg	Ala	Gly	Ser 25	Ser	Thr	Lys	Phe	Thr 30	Ala	Asn
Ala	Leu	Ala 35	Leu	Gly	Ser	Arg	Met 40	Ala	Thr	Thr	Val	Pro 45	Asp	Gly	Cys
Arg	Asn 50	Gly	Leu	Lys	Ser	Lys 55	Tyr	Tyr	Arg	Leu	Cys 60	Asp	Lys	Ala	Glu
Ala 65	Trp	Gly	Ile	Val	Leu 70	Glu	Thr	Val	Ala	Thr 75	Ala	Gly	Val	Val	Thr 80

Ser	Val	Ala	Phe	Met 85	Leu	Thr	Leu	Pro	Ile 90	Leu	Val	Cys	Lys	Val 95	Gln
Asp	Ser	Asn	Arg 100	Arg	Lys	Met	Leu	Pro 105	Thr	Gln	Phe	Leu	Phe 110	Leu	Leu
Gly	Val	Leu 115	Gly	Ile	Phe	Gly	Leu 120	Thr	Phe	Ala	Phe	Ile 125	Ile	Gly	Leu
Asp	Gly 130	Ser	Thr	Gly	Pro	Thr 135	Arg	Phe	Phe	Leu	Phe 140	Gly	Ile	Leu	Phe
Ser 145	Ile	Cys	Phe	Ser	Cys 150	Leu	Leu	Ala	His	Ala 155	Val	Ser	Leu	Thr	Lys 160
Leu	Val	Arg	Gly	Arg 165	Lys	Pro	Leu	Ser	Arg 170	Leu	Val	Ile	Leu	Gly 175	Leu
Ala	Val	Gly	Phe 180	Ser	Leu	Val	Gln	Asp 185	Val	Ile	Ala	Ile	Glu 190	Tyr	Ile
Val	Leu	Thr 195	Met	Asn	Arg	Thr	Lys 200								

&lt;210&gt; 191

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 191

Ala 1	Glu	Ala	His	Gly 5	Gln	Thr	Gln	Asn	His 10	Gln	Pro	Gly	Lys	Gly 15	Leu
Pro	Pro	Pro	Asp 20	Glu	Leu	Gly	Gln	Thr 25	Asp	Ser	Met	Ser	Gln 30	Gln	Ala
Gly	Glu	Ala 35	Asp	Gly	Lys	Glu	Asp 40	Pro	Lys	Glu	Glu	Glu 45	Ala	Cys	Gly
Pro	Cys 50	Ala	Pro	Val	Gln	Ser 55	Asp	Asp	Glu	Gly	Glu 60	Gly	Glu	Ala	Lys
Asp 65	Ala	Gln	His	Thr	Gln 70	Glu	Glu	Glu	Lys	Leu 75	Ser	Arg	Gln	His	Phe 80
Ser	Pro	Val	Gly	Val 85	Leu	His	Leu	Ala	Asp 90	Glu	Asp	Arg	Glu	Ser 95	Glu
His	Glu	Gly	His 100	Arg	Gly	His	Asn	Pro 105	Gly	Cys	Gly	His	Arg 110	Phe	

&lt;210&gt; 192

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 192

Glu 1	Ile	Tyr	Trp	Glu 5	Thr	Asp	Tyr	Asn	His 10	Ser	Gly	Thr	Ile	Asp 15	Ala
His	Glu	Met	Arg	Thr	Ala	Leu	Arg	Lys	Ala	Gly	Phe	Thr	Leu	Asn	Ser

			20					25					30			
Gln	Val	Gln	Gln	Thr	Ile	Ala	Leu	Arg	Tyr	Ala	Cys	Ser	Lys	Leu	Gly	
		35					40					45				
Ile	Asn	Phe	Asp	Ser	Phe	Val	Ala	Cys	Met	Ile	Arg	Leu	Glu	Thr	Leu	
	50					55					60					
Phe	Lys	Leu	Phe	Ser	Leu	Leu	Asp	Glu	Asp	Lys	Asp	Gly	Met	Val	Gln	
65					70					75					80	
Leu	Ser	Leu	Ala	Glu	Trp	Leu	Cys	Cys	Val	Leu	Val					
				85					90							

<210> 193  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<400> 193

Glu	Ser	Leu	Ile	Ala	Phe	Leu	Phe	Leu	His	Asp	Gln	Cys	Ala	Gln	Asp	
1				5					10					15		
Ser	Ile	Val	Leu	Thr	Met	Ile	Lys	Asp	Val	Val	Arg	Ile	Gln	Trp	Thr	
			20					25					30			
Arg	Asn	Glu	Cys	Lys	Gly	Gly	Leu	Glu	Gln	Arg	Arg	Gly	Cys	Pro	Glu	
		35					40					45				
Gly	Lys	Glu	Ser	Tyr	Gln	Ile	Leu	Leu	Asn	Leu	Gln	Pro	Glu	Arg	Leu	
	50					55					60					
Glu	Phe	His	Arg	Pro	Gln	Ser	Ala	Pro	Phe	His	Cys	Ser	Arg	His	Ile	
65					70					75					80	
Lys																

<210> 194  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 194

Lys	Thr	Thr	Ile	His	Gly	Pro	Cys	Gln	Asn	His	Leu	Pro	Pro	Pro	His	
1				5					10					15		
Cys	Phe	Leu	Lys	Arg	Pro	Gly	Thr	Leu	Ser	Lys	Gly	Asp	Pro	Ile	Asp	
			20					25					30			
Ser	Ser	Gln	Glu	Gly	Phe	Arg	Ala	Ser	Ile	Arg	Ala	Trp	Pro	Val	Leu	
		35					40					45				
Ala	Pro	Leu	Leu	Ser	Glu	Gln	Gln	Gly	Phe	Gln	Gly	Ser	Gly	Trp	His	
	50					55					60					
Glu	Ser	Leu	Ser	Leu	Pro	Ser	Cys	Ser	Phe	Met	Thr	Asn	Val	Pro	Arg	
65					70					75					80	
Thr	Gln															

<210> 195

<211> 25  
 <212> PRT  
 <213> Homo sapiens

<400> 195

Arg	Pro	Pro	Pro	Ser	Ser	Arg	Ser	Ser	Leu	Ala	Gly	Gln	Thr	Asn	Thr
1				5					10					15	
Gln	His	Ser	His	Ser	Ala	Arg	Glu	Ser							
			20					25							

<210> 196  
 <211> 71  
 <212> PRT  
 <213> Homo sapiens

<400> 196

Thr	Met	Pro	Ser	Leu	Ser	Ser	Ser	Arg	Arg	Leu	Asn	Ser	Leu	Lys	Arg
1				5					10					15	
Val	Ser	Arg	Arg	Ile	Ile	Gln	Ala	Thr	Lys	Leu	Ser	Lys	Leu	Met	Pro
			20					25					30		
Ser	Leu	Leu	His	Ala	Tyr	Arg	Arg	Ala	Met	Val	Cys	Cys	Thr	Trp	Leu
		35					40					45			
Leu	Arg	Val	Lys	Pro	Ala	Phe	Leu	Arg	Ala	Val	Leu	Ile	Ser	Trp	Ala
	50					55					60				
Ser	Met	Val	Pro	Glu	Trp	Leu									
65					70										

<210> 197  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 197

Ile	Arg	Arg	Asn	Thr	Ser	Arg	Ile	Ser	Val	His	Thr	Trp	Arg	Arg	Thr
1				5					10					15	
Pro	Pro	Tyr	Asp	Ser	Pro	Ala	Cys	Phe	Ser	Cys	Ser	Ile	Val	Ser	Leu
			20					25					30		
Glu	Gly	Ser	Gly	Phe	Phe	Ser	Cys	Val	Ser	Val	Phe	Phe	Ser	Phe	Asp
		35					40					45			
Leu	Ser	Asn	Phe	Ser	Ile	Ser	Ala	Ile	Ser	Gly	Leu	Ser	Asp	Met	Val
	50					55					60				
Ala	Glu	Glu	Lys	Gln	Ser	Glu	Ala	His	Glu	Tyr	Glu	Arg	Gln	Phe	Leu
65					70					75					80
Ala	Ser	Arg	Arg	Ser	Gly										
				85											

<210> 198  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 198

His 1	Pro	Phe	Ser	Thr 5	Phe	Pro	Thr	Leu	Pro 10	Pro	Gln	Ala	Gly	Lys 15	Phe
Asp	Ala	Thr	Leu 20	Leu	Ala	Ser	Gln	Cys 25	Ile	Leu	Gly	Gly	Ala 30	Arg	Leu
Leu	Thr	Ile 35	Arg	Leu	Leu	Ala	Ser 40	Pro	Val	Gln	Ser	Phe 45	Leu	Trp	Lys
Ala	Val 50	Asp	Phe	Ser	Leu	Ala 55	Ser	Leu	Ser	Ser	Ser 60	Val	Ser	Thr	Tyr
Arg 65	Ile	Ser	Arg	Ser	Gln 70	Pro	Tyr	Arg	Val	Cys 75	Gln	Thr	Trp	Leu	Arg 80
Arg	Lys	Ser	Lys	Ala 85	Arg	Arg	Thr	Ser	Thr 90	Ser	Asp	Ser	Ser	Ser 95	Arg
Leu	Ala	Ala	Val 100	Ala											

&lt;210&gt; 199

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 199

Thr 1	Pro	Phe	Pro	Pro 5	Ser	Gln	Leu	Tyr	Pro 10	Leu	Lys	Gln	Val	Asn 15	Ser
Thr	Gln	His	Phe 20	Ser	His	Leu	Ser	Ala 25	Tyr	Leu	Ala	Ala	His 30	Ala	Ser
Leu	Arg	Phe 35	Ala	Cys	Leu	Leu	Leu 40	Leu	Phe	Asn	Arg	Phe 45	Phe	Gly	Arg
Gln	Trp 50	Ile	Phe	Leu	Leu	Arg 55	Leu	Cys	Leu	Leu	Gln 60	Phe	Arg	Leu	Ile
Glu 65	Phe	Leu	Asp	Leu	Ser 70	His	Ile	Gly	Phe	Val 75	Arg	His	Gly	Cys	Gly 80
Gly	Lys	Ala	Lys	Arg 85	Gly	Ala	Arg	Val	Arg 90	Ala	Thr	Val	Pro	Arg 95	Val
Ser	Pro	Gln	Trp 100												

&lt;210&gt; 200

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 200

Gly 1	Leu	Thr	Asp	Gln 5	Tyr	Leu	Glu	Leu	Asn 10	Ala	Leu	Gln	Glu	Glu 15	Leu
Gly	Pro	Phe	Gly	Leu	Val	Ile	Leu	Gly	Phe	Pro	Ser	Asn	Gln	Phe	Gly

20						25						30			
Lys	Gln	Glu	Pro	Gly	Glu	Asn	Ser	Glu	Ile	Leu	Pro	Ser	Leu	Lys	Tyr
		35					40					45			
Val	Arg	Pro	Gly	Gly	Gly	Phe	Val	Pro	Asn	Phe	Gln	Leu	Phe	Glu	Lys
	50					55					60				
Gly	Asp	Val	Asn	Gly	Glu	Lys	Glu	Gln	Lys	Phe	Tyr	Thr	Phe	Leu	Lys
65					70					75					80
Asn	Ser	Cys	Pro	Pro	Thr	Ala	Glu	Leu	Leu	Gly	Ser	Pro	Gly	Arg	Leu
				85					90					95	
Phe	Trp	Glu	Pro	Met	Lys	Ile	His	Asp	Ile	Arg	Trp	Asn	Phe	Glu	Lys
			100					105					110		
Phe	Leu	Val	Gly	Pro	Asp	Gly	Ile	Pro	Val	Met	Arg	Trp	Tyr	His	Arg
		115					120					125			
Thr	Thr	Val	Ser	Asn	Val	Lys	Met	Asp	Ile	Leu	Ser	Tyr	Met	Arg	Arg
	130					135					140				
Gln	Ala	Ala	Leu	Ser	Ala	Arg	Gly	Lys							
145					150										
<210> 201															
<211> 249															
<212> PRT															
<213> Homo sapiens															
<400> 201															
Leu	Met	Pro	Pro	Pro	Tyr	Pro	Tyr	Pro	Leu	Pro	Ile	Met	Gln	Gly	Pro
1				5					10					15	
Arg	Arg	Gly	Ser	Ser	Gly	Arg	Lys	Pro	His	Ser	Gln	Ser	Phe	Tyr	Pro
			20					25					30		
His	Pro	Arg	Phe	Ser	Phe	Leu	Leu	His	Lys	Arg	Gln	Ala	Trp	His	Asn
		35					40					45			
Cys	Val	Ser	Glu	Pro	Leu	Trp	Thr	Arg	Asp	Asn	Cys	Pro	Ser	Val	Cys
	50					55					60				
Met	Ala	Thr	Gln	Pro	Arg	Ile	Cys	Leu	Leu	Glu	Thr	Gln	Gly	Trp	Ser
65					70					75					80
Ile	Cys	Val	Tyr	Gly	Leu	Ala	Gln	His	Pro	His	Ile	Phe	Phe	Ser	Phe
				85					90					95	
Leu	Phe	Gln	Met	Ser	Pro	Lys	Glu	Thr	Gln	Val	Leu	Gly	Pro	Met	Val
			100					105					110		
Leu	Leu	Lys	Pro	Glu	His	His	Ser	Trp	Gly	Gln	His	Leu	Pro	His	Ala
		115					120					125			
His	Thr	Thr	His	His	Gln	Pro	Pro	Ser	Ser	Phe	Leu	Lys	Asp	Pro	Pro
	130					135					140				
Glu	Pro	Pro	Ser	Pro	Ser	His	Ser	Ala	Pro	Glu	Thr	Ser	Gln	Asp	Asn
145					150					155					160



Cys	Glu	Arg	Asp	Gly 165	Arg	Val	Pro	Gln	Val 170	Arg	Gly	Gly	Val	Ser 175	Met
Lys	Glu	Gly	Pro 180	Glu	Ala	Leu	Val	Gly 185	Gly	Pro	Pro	Leu	Ser 190	Pro	Ser
Val	Val	Pro 195	Ala	Leu	Ser	Ala	Phe 200	Arg	Leu	Arg	Leu	Pro 205	Gly	Arg	Asp
Thr	Thr 210	Pro	Ala	Pro	Leu	Glu 215	Asp	Met	Leu	Ser	Ser 220	His	Ser	Val	His
Trp 225	Tyr	Leu	Asn	Thr	Pro 230	Ile	Cys	Pro	Val	Lys 235	Val	Phe	Leu	Gln	Gln 240
Lys	Lys	Lys	Arg	Lys 245	Lys	Lys	Lys	Lys							

&lt;210&gt; 202

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

Ala 1	Gly	Leu	Ser	Ala 5	Pro	Pro	Pro	Ala	Pro 10	Leu	Leu	Cys	Arg	Ala 15	Gln
Ala	Pro	Leu	Ala 20	Leu	Gly	Pro	Asn	Phe 25	Ser	Tyr	Arg	His	Gly 30	Val	Arg
Pro	Gly	Ser 35	Ser	Pro	Gly	Ala	His 40	Leu	Pro	Glu	Ala	Arg 45	Cys	Gly	Gly
Gly	Pro 50	Arg	Gly	Arg	Ser	Gln 55	Ala	Gln	Ser	Pro	Gln 60	Ser	Ser	Gly	Pro
Val 65	Gly	Gly	Arg	Gly	Arg 70	Ser	Gly	Ser	Lys	Ala 75	Arg	Thr	Pro	Gln	Leu 80
Phe	Arg	Leu	Gln	Gln 85	Gln	Leu	Gln	Arg	Phe 90	Gly	His	Gly	Cys	Glu 95	Val
Pro	Arg	Cys	Trp 100	Leu	Gln	Ala	Ala	Arg 105	Glu	His	Pro	Gly	Gln 110	Gly	Gln
Glu	Ala	Gln 115	Ser	Glu	Glu	Glu	Gly 120	Glu	Gly	Gln	Glu	Gly 125	Glu	Gly	Gln
Glu	Glu 130	Gly	Gly	Ser	Pro	Leu 135	Lys	Gly	Pro	Gly	Gln 140	Gly	Ser	Leu	Asn
Leu 145	Pro	Leu	Cys	Leu	Arg 150	Val	Pro	Thr	Thr	Trp 155	Ser				

&lt;210&gt; 203

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

Asp	Pro	Thr	Ser	Leu	Thr	Ala	Met	Glu	Phe	Asp	Leu	Gly	Ala	Ala	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1				5				10				15			
Glu	Pro	Thr	Ser 20	Gln	Lys	Pro	Gly	Val 25	Gly	Ala	Gly	His	Gly 30	Gly	Asp
Pro	Lys	Leu 35	Ser	Pro	His	Lys	Val 40	Gln	Gly	Arg	Ser	Glu 45	Ala	Gly	Ala
Gly	Pro 50	Gly	Pro	Lys	Gln	Gly 55	His	His	Ser	Ser	Ser 60	Asp	Ser	Ser	Ser
Ser 65	Ser	Ser	Asp	Ser	Asp 70	Thr	Asp	Val	Lys	Ser 75	His	Ala	Ala	Gly	Ser 80
Lys	Gln	His	Glu	Ser 85	Ile	Pro	Gly	Lys	Ala 90	Lys	Lys	Pro	Lys	Val 95	Lys
Lys	Lys	Glu	Lys 100	Gly	Lys	Lys	Glu	Lys 105	Gly	Lys	Lys	Lys	Glu 110	Ala	Pro

His

&lt;210&gt; 204

&lt;211&gt; 162

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

Gly 1	Gly	Pro	Pro	Pro 5	Pro	Lys	His	Leu	Ser 10	Ser	Arg	Trp	Leu	Val 15	Leu
Val	Gly	Arg	Glu 20	Glu	Gly	Leu	Met	Ser 25	Pro	Val	Gln	Gly	Pro 30	Ser	Val
Gly	Ser	Leu 35	Leu	Leu	Leu	Ala	Leu 40	Leu	Leu	Leu	Ala	Leu 45	Leu	Leu	Leu
Leu	His 50	Phe	Gly	Leu	Leu	Gly 55	Leu	Ala	Arg	Asp	Ala 60	Leu	Val	Leu	Leu
Gly 65	Ala	Ser	Ser	Val	Gly 70	Leu	His	Ile	Arg	Val 75	Arg	Ile	Ala	Gly	Ala 80
Ala	Ala	Gly	Val	Gly 85	Arg	Ala	Val	Val	Ser 90	Leu	Leu	Trp	Thr	Arg 95	Thr
Cys	Pro	Cys	Leu 100	Arg	Pro	Ala	Leu	Asn 105	Phe	Val	Gly	Thr	Glu 110	Leu	Gly
Ile	Ser	Pro 115	Val	Ala	Arg	Pro	His 120	Thr	Gly	Leu	Leu	Gly 125	Gly	Gly	Leu
Gln	Gly 130	Cys	Ser	Gln	Val	Glu 135	Leu	His	Gly	Gly	Lys 140	Arg	Ser	Trp	Val
Leu 145	Arg	Pro	Arg	Ala	Pro 150	Gly	Pro	Cys	Arg	Gly 155	Ala	Glu	Gln	Gly	Glu 160
Glu	Arg														

&lt;210&gt; 205

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

Val 1	Glu	Pro	Trp	Thr 5	Thr	Cys	Arg	Ala	Ala 10	Gly	Ala	Val	Met	Ala 15	Asp	
Tyr	Trp	Lys	Ser 20	Gln	Pro	Lys	Lys	Phe 25	Cys	Asp	Tyr	Cys	Lys 30	Cys	Trp	
Ile	Ala	Asp 35	Asn	Arg	Pro	Ser	Val 40	Glu	Phe	His	Glu	Arg 45	Gly	Lys	Asn	
His	Lys 50	Glu	Asn	Val	Ala	Lys 55	Arg	Ile	Ser	Glu	Ile 60	Lys	Gln	Lys	Ser	
Leu 65	Asp	Lys	Ala	Lys	Glu 70	Glu	Glu	Lys	Ala	Ser 75	Lys	Glu	Phe	Ala	Ala 80	
Met	Glu	Ala	Ala	Ala 85	Leu	Lys	Ala	Tyr	Gln 90	Glu	Asp	Leu	Lys	Arg 95	Leu	
Gly	Leu	Glu	Ser 100	Glu	Ile	Leu	Glu	Pro 105	Ser	Ile	Thr	Pro	Val 110	Thr	Ser	
Thr	Ile	Pro 115	Pro	Thr	Ser	Thr	Ser 120	Asn	Gln	Gln	Lys	Glu 125	Lys	Lys	Glu	
Lys	Lys 130	Lys	Lys	Arg	Ser	Phe 135	Lys	Gly	Gln	Met	Gly 140	Arg	Arg	His	Asn	
Leu 145																

&lt;210&gt; 206

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 206

Pro 1	Ala	Leu	Ser	His 5	Leu	Pro	Arg	His	Gln 10	Ile	Asn	Arg	Lys	Lys 15	Arg	
Lys	Arg	Arg	Arg 20	Lys	Lys	Asp	Pro	Ser 25	Lys	Gly	Arg	Trp	Val 30	Glu	Gly	
Ile	Thr	Ser 35	Glu	Gly	Tyr	His	Tyr 40	Tyr	Tyr	Asp	Leu	Ile 45	Ser	Gly	Ala	
Ser	Gln 50	Trp	Glu	Lys	Pro	Glu 55	Gly	Phe	Gln	Gly	Asp 60	Leu	Lys	Lys	Thr	
Ala 65	Val	Lys	Thr	Val	Trp 70	Val	Glu	Gly	Leu	Ser 75	Glu	Asp	Gly	Phe	Thr 80	
Tyr	Tyr	Tyr	Asn	Thr 85	Glu	Thr	Gly	Glu	Ser 90	Arg	Trp	Glu	Lys	Pro 95	Asp	
Asp	Phe	Ile	Pro 100	His	Thr	Ser	Asp	Leu 105	Pro	Ser	Ser	Lys	Val 110	Asn	Glu	

[illegible][illegible]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

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1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible][illegible]

20								25				30					
Leu	Leu	Leu	Glu	Leu	Trp	Gln	Met	Glu	Trp	Pro	Gln	Ser	Ser	Lys	Arg		
		35					40					45					
Glu	Glu	Leu	Glu	Asn	Gly	Lys	Ile	Leu	Gly	Lys	Phe	Lys	Gly	Asn	Glu		
	50					55					60						
Val	Met	Ile	Gln														
65																	
<210> 209																	
<400> 209																	
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<212> PRT																	
<213> Homo sapiens																	
<400> 210																	
Ser	Val	His	Cys	Phe	Arg	Glu	Asp	Lys	Met	Lys	Phe	Thr	Ile	Val	Phe		
1				5					10					15			
Ala	Gly	Leu	Leu	Gly	Val	Phe	Leu	Ala	Pro	Ala	Leu	Ala	Asn	Tyr	Asn		
			20					25					30				
Ile	Asn	Val	Asn	Asp	Asp	Asn	Asn	Asn	Ala	Gly	Ser	Gly	Gln	Gln	Ser		
		35					40					45					
Val	Ser	Val	Asn	Asn	Glu	His	Asn	Val	Ala	Asn	Val	Asp	Asn	Asn	Asn		
	50					55					60						
Gly	Trp	Asp	Ser	Trp	Asn	Ser	Ile	Trp	Asp	Tyr	Gly	Asn	Gly	Phe	Ala		
65					70					75					80		
Ala	Thr	Arg	Leu	Phe	Gln	Lys	Lys	Thr	Cys	Ile	Val	His	Lys	Met	Asn		
				85					90					95			
Lys	Glu	Val	Met	Pro	Ser	Ile	Gln	Ser	Leu	Asp	Ala	Leu	Val	Lys	Glu		
			100					105					110				
Lys	Lys	Leu	Gln	Gly	Lys	Gly	Pro	Gly	Gly	Pro	Pro	Pro	Lys	Gly	Leu		
		115					120					125					
Met	Tyr	Ser	Val	Asn	Pro	Asn	Lys	Val	Asp	Asp	Leu	Ser	Lys	Phe	Gly		
	130					135					140						
Lys	Asn	Ile	Ala	Asn	Met	Cys	Arg	Gly	Ile	Pro	Thr	Tyr	Met	Ala	Glu		
145					150					155					160		
Glu	Met	Gln	Glu	Ala	Ser	Leu	Phe	Phe	Tyr	Ser	Gly	Thr	Cys	Tyr	Thr		
				165					170					175			
Thr	Ser	Val	Leu	Trp	Ile	Val	Asp	Ile	Ser	Phe	Cys	Gly	Asp	Thr	Val		
			180					185					190				
Glu	Asn																
<210> 211																	
<211> 82																	
<212> PRT																	

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

Val 1	His	Gln	Ala	Leu 5	Gly	Arg	Trp	Ser	Ser 10	Trp	Ser	Leu	Thr	Leu 15	Lys	
Leu	Leu	Phe	Leu 20	Asp	Gln	Cys	Ile	Lys 25	Gly	Leu	Asn	Gly	Gly 30	His	Asp	
Phe	Leu	Val 35	His	Phe	Val	His	Asn 40	Ala	Cys	Leu	Leu	Leu 45	Lys	Glu	Ser	
Gly	Cys 50	Ser	Lys	Ala	Ile	Ser 55	Ile	Ile	Pro	Asp	Gly 60	Ile	Pro	Gly	Val	
Pro 65	Ser	Val	Val	Ile	Val 70	Asn	Ile	Gly	His	Ile 75	Val	Phe	Ile	Val	Asp 80	
Thr	His															

&lt;210&gt; 212

&lt;211&gt; 119

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 212

Glu 1	Leu	Gly	Leu	Asn 5	His	Leu	Trp	Leu	Arg 10	Val	Trp	Leu	Glu	Pro 15	Thr	
Ala	Gln	Val	Pro 20	Asp	Val	Leu	Phe	Pro 25	Glu	Phe	Met	Glu	Arg 30	Glu	Glu	
Lys	Ala	Val 35	Ser	Leu	Leu	Leu	Trp 40	Phe	Asn	Val	Lys	Glu 45	Pro	Gln	Leu	
Pro	Pro 50	Leu	Pro	Gly	Arg	Glu 55	Ala	Phe	Gly	Phe	Leu 60	Leu	Leu	Leu	Leu	
Ala 65	Leu	Val	Ala	Gly	Glu 70	Val	Leu	Gln	Asp	His 75	Arg	Leu	Ala	Leu	Gln 80	
Leu	Val	Leu	Ala	Gly 85	Leu	Arg	Ala	His	Ala 90	Gly	Arg	Leu	Arg	Phe 95	Arg	
Lys	Ala	Leu	Thr 100	Lys	Ala	Ser	Ala	Arg 105	Cys	Ala	Pro	Glu	Gly 110	Trp	Thr	
Ser	Glu	Ser 115	Phe	Ala	Ser	Phe										

&lt;210&gt; 213

&lt;211&gt; 136

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 213

Ile 1	Ile	Cys	Gly	Cys 5	Val	Ser	Gly	Leu	Ser 10	Pro	Leu	His	Arg	Ser 15	Leu	
Met	Tyr	Cys	Phe	Gln	Ser	Ser	Trp	Arg	Gly	Arg	Lys	Arg	Leu	Tyr	Leu	

20								25				30			
Cys	Cys	Ser	Gly	Leu	Met	Ser	Lys	Ser	Arg	Ser	Ser	Leu	Leu	Cys	Leu
		35					40					45			
Ala	Glu	Lys	Pro	Leu	Ala	Phe	Phe	Phe	Phe	Ser	Leu	Arg	Leu	Trp	Arg
	50					55					60				
Val	Lys	Tyr	Ser	Arg	Thr	Thr	Ala	Leu	Arg	Cys	Ser	Trp	Ser	Ser	Arg
	65				70					75					80
Ala	Cys	Gly	Leu	Met	Arg	Gly	Val	Cys	Ala	Ser	Gly	Arg	Pro	Ser	Arg
				85					90					95	
Arg	Pro	Arg	Pro	Ala	Val	Leu	Leu	Lys	Ala	Gly	His	Arg	Ser	His	Ser
			100					105					110		
Pro	Leu	Ser	Glu	Thr	Met	His	Gly	Arg	Ser	His	Ser	Ser	Phe	Ser	Asp
		115					120					125			
Arg	Phe	Arg	Arg	Ser	Leu	Met	Thr								
	130					135									

&lt;210&gt; 214

&lt;211&gt; 101

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 214

Thr	Leu	Glu	Thr	Val	His	Gln	Gly	Pro	Val	Gln	Trp	Ala	Gln	Ala	Arg
1				5					10					15	
His	Ala	Ala	Thr	Asp	Asp	Ser	Gly	Gln	Ala	Leu	Lys	Gly	Arg	Ser	Ser
			20					25					30		
Arg	Gly	Tyr	Tyr	Phe	Ser	Asp	Lys	Ile	Gln	Met	Pro	Leu	Leu	Cys	Gly
		35					40					45			
Tyr	Tyr	Arg	Asn	Pro	Ser	Thr	Gly	Asn	Lys	Ala	His	Phe	Gln	Asn	Tyr
	50					55					60				
His	Gln	Arg	Arg	Pro	Pro	Glu	Ser	Tyr	Pro	Gln	Ala	Lys	Leu	Arg	Val
	65				70					75					80
His	Cys	Gly	Asn	Arg	Trp	Leu	Tyr	Phe	Leu	His	Leu	Arg	Glu	Gln	Ile
				85					90					95	
Pro	Ala	Ser	Val	Lys											
			100												

&lt;210&gt; 215

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 215

Leu	Arg	Cys	Pro	Ala	Phe	Arg	Ser	Thr	Ala	Gly	Arg	Gly	Leu	Arg	Glu
1				5					10					15	
Gly	Leu	Pro	Glu	Ala	Gln	Thr	Pro	Arg	Met	Ser	Pro	Gln	Ala	Arg	Glu
			20					25					30		

Asp	Gln	Leu 35	Gln	Arg	Lys	Ala	Val 40	Val	Leu	Glu	Tyr	Phe 45	Thr	Arg	His
Lys	Arg 50	Lys	Glu	Lys	Lys	Lys 55	Lys	Ala	Lys	Gly	Phe 60	Ser	Ala	Arg	Gln
Arg 65	Arg	Glu	Leu	Arg	Leu 70	Phe	Asp	Ile	Lys	Pro 75	Glu	Gln	Gln	Arg	Tyr 80
Ser	Leu	Phe	Leu	Pro 85	Leu	His	Glu	Leu	Trp 90	Lys	Gln	Tyr	Ile	Arg 95	Asp
Leu	Cys	Ser	Gly 100	Leu	Lys	Pro	Asp	Thr 105	Gln	Pro	Gln	Met	Ile 110	Gln	Ala
Lys	Leu	Leu 115	Lys	Ala	Asp	Leu	His 120	Gly	Ala	Ile	Ile	Ser 125	Val	Thr	Lys
Ser	Lys 130	Cys	Pro	Ser	Tyr	Val 135	Gly	Ile	Thr	Gly	Ile 140	Leu	Leu	Gln	Glu
Thr 145	Lys	His	Ile	Phe	Lys 150	Ile	Ile	Thr	Lys	Glu 155	Asp	Arg	Leu	Lys	Val 160
Ile	Pro	Lys	Leu	Asn 165	Cys	Val	Phe	Thr	Val 170	Glu	Thr	Asp	Gly	Phe 175	Ile
Ser	Tyr	Ile	Tyr 180	Gly	Ser	Lys	Phe	Gln 185	Leu	Arg	Ser	Ser	Glu 190	Arg	Ser
Ala	Lys	Lys 195	Phe	Lys	Ala	Lys	Gly 200	Thr	Ile	Asp	Leu				
<210> 216															
<211> 645															
<212> PRT															
<213> Homo sapiens															
<400> 216															
Pro 1	Thr	Arg	Pro	Val 5	Ala	Ala	Gly	Ser	Glu 10	Gln	Gln	Gln	Gln	Ser 15	Ala
Phe	Ile	Gln	Glu 20	Arg	Gln	Pro	Val	Ala 25	Leu	Met	Arg	Leu	Leu 30	Ser	Phe
Asn	Val	Pro 35	His	Ile	Lys	Asn	Ser 40	Thr	Gly	Glu	Pro	Ile 45	Trp	Lys	Val
Leu	Ile 50	Tyr	Asp	Arg	Phe	Gly 55	Gln	Asp	Ile	Ile	Ser 60	Pro	Leu	Leu	Ser
Val 65	Lys	Glu	Leu	Arg	Asp 70	Met	Gly	Ile	Thr	Leu 75	His	Leu	Leu	Leu	His 80
Ser	Asp	Arg	Asp	Pro 85	Ile	Pro	Asp	Val	Pro 90	Ala	Val	Tyr	Phe	Val 95	Met
Pro	Thr	Glu	Glu 100	Asn	Ile	Asp	Arg	Met 105	Cys	Gln	Asp	Leu	Arg 110	Asn	Gln
Leu	Tyr	Glu	Ser	Tyr	Tyr	Leu	Asn	Phe	Ile	Ser	Ala	Ile	Ser	Arg	Ser



	115					120					125				
Lys	Leu 130	Glu	Asp	Ile	Ala	Asn 135	Ala	Ala	Leu	Ala	Ala 140	Ser	Ala	Val	Thr
Gln 145	Val	Ala	Lys	Val	Phe 150	Asp	Gln	Tyr	Leu	Asn 155	Phe	Ile	Thr	Leu	Glu 160
Asp	Asp	Met	Phe	Val 165	Leu	Cys	Asn	Gln	Asn 170	Lys	Glu	Leu	Val	Ser 175	Tyr
Arg	Ala	Ile	Asn 180	Arg	Pro	Asp	Ile	Thr 185	Asp	Thr	Glu	Met	Glu 190	Thr	Val
Met	Asp	Thr 195	Ile	Val	Asp	Ser	Leu 200	Phe	Cys	Phe	Phe	Val 205	Thr	Leu	Gly
Ala	Val 210	Pro	Ile	Ile	Arg	Cys 215	Ser	Arg	Gly	Thr	Ala 220	Ala	Glu	Met	Val
Ala 225	Val	Lys	Leu	Asp	Lys 230	Lys	Leu	Arg	Glu	Asn 235	Leu	Arg	Asp	Ala	Arg 240
Asn	Ser	Leu	Phe	Thr 245	Gly	Asp	Thr	Leu	Gly 250	Ala	Gly	Gln	Phe	Ser 255	Phe
Gln	Arg	Pro	Leu 260	Leu	Val	Leu	Val	Asp 265	Arg	Asn	Ile	Asp	Leu 270	Ala	Thr
Pro	Leu	His 275	His	Thr	Trp	Thr	Tyr 280	Gln	Ala	Leu	Val	His 285	Asp	Val	Leu
Asp	Phe 290	His	Leu	Asn	Arg	Val 295	Asn	Leu	Glu	Glu	Ser 300	Ser	Gly	Val	Glu
Asn 305	Ser	Pro	Ala	Gly	Ala 310	Arg	Pro	Lys	Arg	Lys 315	Asn	Lys	Lys	Ser	Tyr 320
Asp	Leu	Thr	Pro	Val 325	Asp	Lys	Phe	Trp	Gln 330	Lys	His	Lys	Gly	Ser 335	Pro
Phe	Pro	Glu	Val 340	Ala	Glu	Ser	Val	Gln 345	Gln	Glu	Leu	Glu	Ser 350	Tyr	Arg
Ala	Gln	Glu 355	Asp	Glu	Val	Lys	Arg 360	Leu	Lys	Ser	Ile	Met 365	Gly	Leu	Glu
Gly	Glu 370	Asp	Glu	Gly	Ala	Ile 375	Ser	Met	Leu	Ser	Asp 380	Asn	Thr	Ala	Lys
Leu 385	Thr	Ser	Ala	Val	Ser 390	Ser	Leu	Pro	Glu	Leu 395	Leu	Glu	Lys	Lys	Arg 400
Leu	Ile	Asp	Leu	His 405	Thr	Asn	Val	Ala	Thr 410	Ala	Val	Leu	Glu	His 415	Ile
Lys	Ala	Arg	Lys 420	Leu	Asp	Val	Tyr	Phe 425	Glu	Tyr	Glu	Glu	Lys 430	Ile	Met
Ser	Lys	Thr 435	Thr	Leu	Asp	Lys	Ser 440	Leu	Leu	Asp	Ile	Ile 445	Ser	Asp	Pro
Asp	Ala	Gly	Thr	Pro	Glu	Asp	Lys	Met	Arg	Leu	Phe	Leu	Ile	Tyr	Tyr

450					455					460					
Ile 465	Ser	Thr	Gln	Gln	Ala 470	Pro	Ser	Glu	Ala	Asp 475	Leu	Glu	Gln	Tyr	Lys 480
Lys	Ala	Leu	Thr	Asp 485	Ala	Gly	Cys	Asn	Leu 490	Asn	Pro	Leu	Gln	Tyr 495	Ile
Lys	Gln	Trp	Lys 500	Ala	Phe	Thr	Lys	Met 505	Ala	Ser	Ala	Pro	Ala 510	Ser	Tyr
Gly	Ser	Thr 515	Thr	Thr	Lys	Pro	Met 520	Gly	Leu	Leu	Ser	Arg 525	Val	Met	Asn
Thr	Gly 530	Ser	Gln	Phe	Val	Met 535	Glu	Gly	Val	Lys	Asn 540	Leu	Val	Leu	Lys
Gln 545	Gln	Asn	Leu	Pro	Val 550	Thr	Arg	Ile	Leu	Asp 555	Asn	Leu	Met	Glu	Met 560
Lys	Ser	Asn	Pro	Glu 565	Thr	Asp	Asp	Tyr	Arg 570	Tyr	Phe	Asp	Pro	Lys 575	Met
Leu	Arg	Gly	Asn 580	Asp	Ser	Ser	Val	Pro 585	Arg	Asn	Lys	Asn	Pro 590	Phe	Gln
Glu	Ala	Ile 595	Val	Phe	Val	Val	Gly 600	Gly	Gly	Asn	Tyr	Ile 605	Glu	Tyr	Gln
Asn	Leu 610	Val	Asp	Tyr	Ile	Lys 615	Gly	Lys	Gln	Gly	Lys 620	His	Ile	Leu	Tyr
Gly 625	Cys	Ser	Glu	Leu	Phe 630	Asn	Ala	Thr	Gln	Phe 635	Ile	Lys	Gln	Leu	Ser 640
Gln	Leu	Gly	Gln	Lys 645											

<210> 217  
 <211> 101  
 <212> PRT  
 <213> Homo sapiens

<400> 217

Gly 1	Ala	Gly	Pro	Ser 5	Gln	Leu	Arg	Leu	His 10	Tyr	Pro	Arg	Ile	Ser 15	Met
Ala	Val	Arg	Gln 20	Trp	Val	Ile	Ala	Leu 25	Ala	Leu	Ala	Ala	Leu 30	Leu	Val
Val	Asp	Arg 35	Glu	Val	Pro	Val	Ala 40	Ala	Gly	Lys	Leu	Pro 45	Phe	Ser	Arg
Met	Pro 50	Ile	Cys	Glu	His	Met 55	Val	Glu	Ser	Pro	Thr 60	Cys	Ser	Gln	Met
Ser 65	Asn	Leu	Val	Cys	Gly 70	Thr	Asp	Gly	Leu	Thr 75	Tyr	Thr	Asn	Glu	Cys 80
Gln	Leu	Cys	Leu	Ala 85	Arg	Ile	Lys	Thr	Lys 90	Gln	Asp	Ile	Gln	Ile 95	Met

Lys Asp Gly Lys Cys  
100

<210> 218  
<211> 123  
<212> PRT  
<213> Homo sapiens

<400> 218

Gln 1	Leu	Gly	Trp	Ile 5	Phe	Tyr	Phe	Met	Ser 10	Tyr	Pro	Leu	His	Ala 15	His
His	Cys	Ser	Pro 20	Ala	Asp	Thr	Ser	Trp 25	Leu	Glu	Val	Leu	Leu 30	Trp	Asp
Gln	His	Leu 35	Pro	Ser	Phe	Met	Ile 40	Trp	Met	Ser	Cys	Leu 45	Val	Phe	Ile
Arg	Ala 50	Lys	Gln	Ser	Trp	His 55	Ser	Phe	Val	Tyr	Val 60	Ser	Pro	Ser	Val
Pro 65	Gln	Thr	Arg	Leu	Asp 70	Ile	Trp	Glu	Gln	Val 75	Gly	Asp	Ser	Thr	Met 80
Cys	Ser	Gln	Met	Gly 85	Ile	Leu	Glu	Lys	Gly 90	Ser	Phe	Pro	Ala	Ala 95	Thr
Gly	Thr	Ser	Leu 100	Ser	Thr	Thr	Arg	Arg 105	Ala	Ala	Lys	Ala	Arg 110	Ala	Ile
Thr	His	Trp 115	Arg	Thr	Ala	Met	Leu 120	Ile	Leu	Gly					

<210> 219  
<211> 64  
<212> PRT  
<213> Homo sapiens

<400> 219

Ile 1	Lys	Ala	Lys	Phe 5	Asn	Leu	Asn	Ala	Phe 10	Phe	Phe	Phe	Phe	Leu 15	Leu
Arg	Ser	Glu	Ile 20	Gly	Thr	Val	Ile	Leu 25	Ser	Thr	Glu	Arg	Gln 30	Thr	Ile
Lys	Trp	Ala 35	Met	Lys	Gly	Gly	Gly 40	Lys	Val	Leu	Ser	Ile 45	Val	Arg	Gly
Ile	Gln 50	Pro	Glu	Ile	Lys	Pro 55	Ile	Tyr	Lys	His	Val 60	Cys	Ser	Ser	Lys

<210> 220  
<211> 67  
<212> PRT  
<213> Homo sapiens

<400> 220

Ser 1	Phe	Ala	Ile	Pro 5	Phe	Pro	Trp	His	Cys 10	Thr	Ile	Ser	Pro	Ile 15	Ile
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Gly	Gln	Ser	Leu 20	Gly	Phe	Leu	Gly	Phe 25	Thr	Met	Val	Ala	Thr 30	Thr	Ile
Arg	Leu	Ile 35	Asp	Gly	Ser	Asn	Leu 40	Lys	Lys	Lys	Val	Met 45	Val	Met	Asp
Lys	Ile 50	Ser	Arg	Ser	Arg	Glu 55	Val	Cys	Tyr	His	Lys 60	Ile	Thr	Val	Ala
Ser 65	Thr	Ser													

<210> 221  
 <211> 117  
 <212> PRT  
 <213> Homo sapiens

<400> 221

Thr 1	Ile	Ile	Ser	Ser 5	Ile	Thr	Asp	Ser	Gln 10	Leu	Gln	Glu	Val	Ala 15	Glu
Gln	Leu	Glu	Ile 20	Phe	Ala	Ala	Leu	His 25	Glu	Val	Leu	His	Ile 30	Ile	Asn
Asp	Arg	Lys 35	Asn	Leu	Lys	Gly	Gly 40	Leu	Gln	Glu	Val	Ala 45	Glu	Gln	Leu
Glu 50	Leu	Glu	Arg	Ile	Gly	Pro 55	Gln	His	Gln	Ala	Gly 60	Ser	Asp	Ser	Leu
Leu 65	Thr	Gly	Met	Ala	Phe 70	Phe	Lys	Met	Arg	Glu 75	Met	Phe	Phe	Glu	Asp 80
His	Ile	Asp	Asp	Ala 85	Lys	Tyr	Cys	Gly	His 90	Leu	Tyr	Gly	Leu	Gly 95	Ser
Gly	Ser	Ser	Tyr 100	Val	Gln	Asn	Gly	Thr 105	Gly	Asn	Ala	Tyr	Glu 110	Glu	Glu
Ala	Asn	Lys 115	Gln	Ser											

<210> 222  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens

<400> 222

Pro 1	Thr	Cys	Pro	Ile 5	Gln	His	Phe	Ile	Met 10	Met	Lys	Leu	Trp	Val 15	Pro
Ser	Arg	Ser	Leu 20	Pro	Asn	Ser	Pro	Asn 25	His	Tyr	Arg	Ser	Phe 30	Leu	Ser
His	Thr	Leu 35	His	Ile	Arg	Tyr	Asn 40	Asn	Ser	Leu	Phe	Ile 45	Ser	Asn	Thr
His 50	Leu	Ser	Arg	Arg	Lys	Leu 55	Arg	Val	Thr	Asn	Pro 60	Ile	Tyr	Thr	Arg
Lys	Arg	Ser	Leu	Asn	Ile	Phe	Tyr	Leu	Leu	Ile	Pro	Ser	Cys	Arg	Thr

65				70				75				80			
Arg	Leu	Ile	Leu	Trp 85	Ile	Ile	Tyr	Ile	Tyr 90	Arg	Asn	Leu	Lys	His 95	Trp
Ser	Thr	Ser	Thr 100	Val	Arg	Ser	His	Ser 105	His	Ser	Ile	Tyr	Arg 110	Leu	Arg
Pro	Ser	Met 115	Arg	Thr	Asn	Ile	Ile 120	Leu	Arg	Cys	His	Ser 125	Tyr	Tyr	Lys
Pro	Pro 130	Ile	Ser	His	Pro	Ile 135	Tyr	Trp	Asn	Asn	Pro 140	Ser	Arg	Met	Asn
Leu 145	Arg	Gly	Leu	Leu	Ser 150	Arg	Gln	Ser	His	Leu 155	Asp	Pro	Ile	Leu	Arg 160
Phe	Pro	Leu	His	Leu 165	Thr	Ile	Tyr	Tyr	Arg 170	Gly	Pro	Ser	Asn	Arg 175	Ser
Pro	Pro	Leu	Pro 180	Pro	Arg	Asn	Arg	Ile 185	Lys	Gln	Pro	Asn	Arg 190	Ile	Lys
Leu	Arg	Cys 195	Arg												
<210> 223															
<211> 174															
<212> PRT															
<213> Homo sapiens															
<400> 223															
Leu 1	Pro	Ser	Ala	Ile 5	Glu	Gly	Pro	Thr	Pro 10	Val	Ser	Ala	Leu	Leu 15	His
Ser	Ser	Thr	Ile 20	Val	Val	Ala	Gly	Ile 25	Phe	Leu	Leu	Val	Arg 30	Phe	His
Pro	Leu	Thr 35	Thr	Asn	Asn	Asn	Phe 40	Ile	Leu	Thr	Thr	Ile 45	Leu	Cys	Leu
Gly	Ala 50	Leu	Thr	Thr	Leu	Phe 55	Thr	Ala	Ile	Cys	Ala 60	Leu	Thr	Gln	Asn
Asp 65	Ile	Lys	Lys	Ile	Ile 70	Ala	Phe	Ser	Thr	Ser 75	Ser	Gln	Leu	Gly	Leu 80
Ile	Ile	Val	Thr	Leu 85	Gly	Ile	Asn	Gln	Pro 90	His	Leu	Ala	Phe	Leu 95	His
Ile	Cys	Thr	His 100	Ala	Phe	Phe	Lys	Ala 105	Ile	Leu	Phe	Ile	Cys 110	Ser	Gly
Ser	Ile	Ile 115	His	Ser	Leu	Ala	Asp 120	Glu	Gln	Asp	Ile	Arg 125	Lys	Ile	Gly
Asn	Ile 130	Thr	Lys	Ile	Ile	Pro 135	Phe	Thr	Ser	Ser	Cys 140	Leu	Val	Ile	Gly
Ser 145	Leu	Ala	Leu	Thr	Gly 150	Ile	Pro	Phe	Leu	Thr 155	Gly	Phe	Tyr	Ser	Lys 160

Asp Leu Ile Ile Glu Ala Ile Asn Thr Cys Asn Thr Asn Ala  
165 170

<210> 224

<211> 123

<212> PRT

<213> Homo sapiens

<400> 224

Phe 1	Leu	Lys	Thr	Thr 5	Ala	Leu	Ile	Ile	Ser 10	Val	Leu	Gly	Phe	Leu 15	Ile
Ala	Leu	Glu	Leu 20	Asn	Asn	Leu	Thr	Ile 25	Lys	Leu	Ser	Ile	Asn 30	Lys	Ala
Asn	Pro	Tyr 35	Ser	Ser	Phe	Ser	Thr 40	Leu	Leu	Gly	Phe	Phe 45	Pro	Ser	Ile
Ile	His 50	Arg	Ile	Thr	Pro	Ile 55	Lys	Ser	Leu	Asn	Leu 60	Ser	Leu	Lys	Thr
Ser 65	Leu	Thr	Leu	Leu	Asp 70	Leu	Ile	Trp	Leu	Glu 75	Lys	Thr	Ile	Pro	Lys 80
Ser	Thr	Ser	Thr	Leu 85	His	Thr	Asn	Ile	Thr 90	Thr	Leu	Thr	Thr	Asn 95	Gln
Lys	Gly	Leu	Ile 100	Lys	Leu	Tyr	Phe	Ile 105	Ser	Phe	Leu	Ile	Asn 110	Ile	Ile
Leu	Ile	Ile 115	Ile	Leu	Tyr	Ser	Ile 120	Asn	Leu	Glu					

<210> 225

<211> 129

<212> PRT

<213> Homo sapiens

<400> 225

Asn 1	Met	Leu	Leu	Ala 5	Glu	Val	Arg	Ile	Ser 10	Met	Val	Ile	Arg	Asn 15	Ser
Val	Arg	Tyr	Leu 20	Met	Asn	Arg	Leu	Met 25	Phe	Gly	Ser	Glu	Cys 30	Ile	Tyr
His	Glu	Glu 35	Asn	Cys	Ile	Ile	Asp 40	His	Val	Thr	Lys	Arg 45	Ala	Thr	Asp
Val	Asn 50	Arg	Ile	Glu	Lys	Lys 55	Ser	Val	Leu	Lys	Leu 60	Ile	Leu	Ser	Ser
Ile 65	Glu	Phe	Met	Val	Thr 70	Gln	Cys	Gln	Val	Val 75	Ile	Ile	Tyr	Ser	Ile 80
Leu	Leu	Trp	Lys	Asn 85	Ile	Asn	Arg	Gly	Lys 90	Arg	Leu	Ile	Met	Lys 95	Glu
Asn	Leu	Ile	Asp 100	Val	Val	Val	Tyr	Ser 105	Gly	Lys	Leu	Met	Cys 110	Leu	Ile
Arg	Phe	Asp	Ile	Glu	Ile	Arg	Ile	Gly	Asp	Ser	Arg	Arg	Met	Lys	Ile

115

120

125

Lys

&lt;210&gt; 226

&lt;211&gt; 83

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 226

Phe 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Ala	Ile	Gln 10	Met	Asn	Val	Tyr	Phe 15	Leu
Asn	Pro	His	Arg 20	Val	Arg	Ala	Glu	Leu 25	Arg	Asp	Ala	Trp	His 30	Ser	Ile
Ser	His	Pro 35	Gly	Ser	Leu	Pro	Arg 40	Ser	Phe	Phe	Phe	Ala 45	Gly	Ser	Ile
Leu	Asp 50	Leu	Tyr	His	Phe	Leu 55	Gln	Arg	Gln	Tyr	Pro 60	Glu	Trp	Gln	Ser
Gln 65	Val	Tyr	Phe	Lys	Val 70	Gly	Val	Phe	Ser	Gly 75	Ser	Arg	Gly	Asp	Trp 80
Ile	Pro	Ser													

&lt;210&gt; 227

&lt;211&gt; 122

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

Ser 1	Met	Met	Leu	Phe 5	Lys	Val	Leu	Val	Ile 10	Thr	Val	Phe	Cys	Gly 15	Leu
Thr	Val	Ala	Phe 20	Pro	Leu	Ser	Glu	Leu 25	Val	Ser	Ile	Asn	Lys 30	Glu	Leu
Gln	Asn	Ser 35	Ile	Ile	Asp	Leu	Leu 40	Asn	Ser	Val	Phe	Asp 45	Gln	Leu	Gly
Ser	Tyr 50	Arg	Gly	Thr	Lys	Ala 55	Pro	Leu	Glu	Asp	Tyr 60	Thr	Asp	Asp	Asp
Leu 65	Ser	Thr	Asp	Ser	Glu 70	Gln	Ile	Met	Asp	Phe 75	Thr	Pro	Ala	Ala	Asn 80
Lys	Gln	Asn	Ser	Glu 85	Phe	Ser	Thr	Asp	Val 90	Glu	Thr	Val	Ser	Ser 95	Gly
Phe	Leu	Glu	Glu 100	Phe	Thr	Glu	Asn	Thr 105	Asp	Ile	Thr	Val	Lys 110	Ile	Pro
Leu	Ala	Gly 115	Asn	Pro	Val	Ser	Pro 120	Thr	Ser						

&lt;210&gt; 228

&lt;211&gt; 62

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 228

Thr 1	Ser	Thr	Thr	Val 5	Phe	Phe	Phe	Pro	Phe 10	His	Leu	Ser	Leu	Pro 15	Val
Gly	Cys	Thr	Val 20	Cys	Ser	His	Ala	Leu 25	Cys	Ile	Asn	Ile	Leu 30	Glu	Ile
Tyr	Arg	Ser 35	Val	Leu	Tyr	Phe	Leu 40	Tyr	Cys	Trp	Ile	Leu 45	Ile	Ile	Lys
Thr	Phe 50	Thr	Arg	Val	Leu	Asn 55	Lys	Ser	Ser	Leu	Thr 60	Arg	Lys		

&lt;210&gt; 229

&lt;211&gt; 99

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

Ala 1	Arg	Pro	Cys	Met 5	Asn	Ser	Thr	Lys	Ala 10	Leu	Pro	His	Gly	Arg 15	Glu
His	Thr	Arg	Leu 20	Lys	Met	Leu	Ser	Tyr 25	Leu	Lys	Asn	Lys	Met 30	Cys	Lys
Ser	Ser	Gly 35	Trp	His	Lys	Thr	Lys 40	Val	Asn	Ala	Ser	Trp 45	Gly	Thr	Phe
Leu	Arg 50	Gly	Leu	Ala	Glu	Cys 55	Val	Asn	Ile	Ile	Asp 60	Phe	Cys	Leu	Cys
Tyr 65	Met	Thr	Ser	Val	Thr 70	Ser	Leu	Lys	Ile	Cys 75	Thr	Ile	Gln	Phe	Gln 80
Leu	Trp	Ile	Thr	Ser 85	Val	Asp	Leu	Cys	Glu 90	Gly	Phe	Tyr	Leu	Cys 95	Arg
Met	Gly	Val													

&lt;210&gt; 230

&lt;211&gt; 63

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

Gly 1	Glu	Leu	Gln	Lys 5	Ser	Ser	His	Tyr	His 10	Pro	Pro	Glu	Leu	Phe 15	Glu
Met	Ile	Phe	Phe 20	Val	His	Phe	Gly	Cys 25	Ser	Ile	Gly	Gly	Arg 30	Ile	Tyr
Tyr	Asn	Met 35	Asp	His	Leu	Tyr	Phe 40	Cys	Ile	Tyr	Leu	Phe 45	Ile	Thr	Arg
Pro	Gln 50	Pro	Gln	Ser	Ser	Phe 55	Ser	Pro	Ser	Thr	Ser 60	Leu	Cys	Leu	

&lt;210&gt; 231

&lt;211&gt; 64



<212> PRT  
 <213> Homo sapiens

<400> 231

Ile	Asn	Lys	Tyr	Arg	Ser	Arg	Asp	Asp	Pro	Tyr	Tyr	Ser	Ile	Phe	Tyr
1				5					10					15	
His	Gln	Tyr	Cys	Ser	Gln	Asn	Val	Gln	Lys	Lys	Ser	Phe	Gln	Ile	Thr
			20					25					30		
Gln	Glu	Asp	Asp	Asn	Gly	Trp	Thr	Phe	Val	Ile	His	Leu	Lys	Asp	Cys
		35					40					45			
Gly	Arg	Ala	Asn	Ser	Thr	His	Cys	Ile	Val	Cys	Ala	Tyr	Gly	Gly	Leu
	50					55					60				

<210> 232

<211> 88

<212> PRT

<213> Homo sapiens

<400> 232

Pro	Leu	Phe	Cys	Ala	Ile	Leu	Lys	Thr	Cys	Thr	Phe	Tyr	Phe	Ser	Asp
1				5					10					15	
Ser	Leu	Thr	Phe	Leu	Ile	Glu	Cys	Val	Leu	Tyr	His	Ala	Val	Met	Leu
			20					25					30		
Trp	Tyr	Tyr	Ser	Tyr	Arg	Val	Leu	Pro	Ile	Leu	Lys	Thr	Cys	His	Phe
		35					40					45			
Pro	Lys	Arg	Ser	Phe	Asp	Ser	Ala	Leu	Glu	Val	Leu	His	Lys	Leu	Lys
	50					55					60				
Ser	Leu	Ser	Asn	Ile	Asn	Met	Lys	Gly	Gly	Thr	Gly	Cys	Asn	Ile	Tyr
65					70					75					80
Ser	Gln	Val	Thr	Ser	Leu	Tyr	Ile								
				85											

<210> 233

<211> 161

<212> PRT

<213> Homo sapiens

<400> 233

Ala	Ser	Thr	Ile	Met	Asp	Leu	Leu	Phe	Gly	Arg	Arg	Lys	Thr	Pro	Glu
1				5					10					15	
Glu	Leu	Leu	Arg	Gln	Asn	Gln	Arg	Ala	Leu	Asn	Arg	Ala	Met	Arg	Glu
			20					25					30		
Leu	Asp	Arg	Glu	Arg	Gln	Lys	Leu	Glu	Thr	Gln	Glu	Lys	Lys	Ile	Ile
		35					40					45			
Ala	Asp	Ile	Lys	Lys	Met	Ala	Lys	Gln	Gly	Gln	Met	Asp	Ala	Val	Arg
	50					55					60				
Ile	Met	Ala	Lys	Asp	Leu	Val	Arg	Thr	Arg	Arg	Tyr	Val	Arg	Lys	Phe
65					70					75					80

Val	Leu	Met	Arg	Ala 85	Asn	Ile	Gln	Ala	Val 90	Ser	Leu	Lys	Ile	Gln 95	Thr
Leu	Lys	Ser	Asn 100	Asn	Ser	Met	Ala	Gln 105	Ala	Met	Lys	Gly	Val 110	Thr	Lys
Ala	Met	Gly 115	Thr	Met	Asn	Arg	Gln 120	Leu	Lys	Leu	Pro	Gln 125	Ile	Gln	Lys
Ile	Met 130	Met	Glu	Phe	Glu	Arg 135	Gln	Ala	Glu	Ile	Met 140	Asp	Met	Lys	Glu
Glu 145	Arg	Ile	Glu	Leu	Leu 150	His	Leu	Met	Ile	Pro 155	Trp	Val	Leu	Gly	Lys 160

Phe

&lt;210&gt; 234

&lt;211&gt; 120

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 234

Arg 1	Arg	Val	Arg	Thr 5	Lys	Ser	Phe	Ala	Met 10	Met	Arg	Thr	Ala	Ser 15	Ile
Trp	Pro	Cys	Leu 20	Ala	Ile	Phe	Leu	Met 25	Ser	Ala	Met	Ile	Phe 30	Phe	Ser
Trp	Val	Ser 35	Ser	Phe	Cys	Arg	Ser 40	Arg	Ser	Ser	Ser	Arg 45	Met	Ala	Arg
Phe	Arg 50	Ala	Leu	Trp	Phe	Cys 55	Arg	Ser	Ser	Ser	Ser 60	Gly	Val	Phe	Arg
Arg 65	Pro	Asn	Asn	Arg	Ser 70	Met	Met	Val	Glu	Ala 75	His	Trp	Gln	Ala	Gly 80
Ala	Gly	Thr	Asp	Thr 85	Arg	Phe	Arg	Phe	Arg 90	Val	Thr	Leu	Leu	Phe 95	Leu
Gly	Ser	Pro	Thr 100	Cys	Pro	Pro	Thr	Lys 105	Ala	Pro	Arg	Ser	Cys 110	Arg	Arg
Arg	Arg	Arg 115	Phe	Arg	Gly	Arg	Val 120								

&lt;210&gt; 235

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 235

Lys 1	Leu	Pro	Gln	Asn 5	Pro	Arg	Asp	His	Gln 10	Met	Gln	Gln	Phe	Asn 15	Pro
Leu	Leu	Leu	His 20	Ile	His	Asp	Leu	Cys 25	Leu	Pro	Leu	Lys	Leu 30	His	His
Asp	Leu	Leu	Asp	Leu	Gly	Gln	Leu	Gln	Leu	Ser	Val	His	Gly	Ala	His

35							40				45				
Gly	Leu	Gly	Asp	Thr	Leu	His	Gly	Leu	Cys	His	Arg	Val	Val	Gly	Leu
	50					55					60				
Glu	Cys	Leu	Asp	Leu	Glu	Gly	His	Ser	Leu	Asp	Val	Gly	Pro	His	Gln
65					70					75					80
Tyr	Lys	Leu	Ala	His	Ile	Ala	Pro	Gly	Ala	His	Gln	Val	Phe	Cys	His
				85					90					95	
Asp	Ala	Asn	Ser	Ile	His	Leu	Ala	Leu	Leu	Gly	His	Leu	Leu	Asn	Val
			100					105					110		
Cys	Asn	Asp	Phe	Leu	Leu	Leu	Gly	Leu							
		115					120								

&lt;210&gt; 236

&lt;211&gt; 180

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

Lys	Thr	Lys	Arg	Ser	Val	Lys	Asp	Ala	Ala	Lys	Lys	Gly	Gln	Lys	Asp
1				5					10					15	
Val	Cys	Ile	Val	Leu	Ala	Lys	Glu	Met	Ile	Arg	Ser	Arg	Lys	Ala	Val
			20					25					30		
Ser	Lys	Leu	Tyr	Ala	Ser	Lys	Ala	His	Met	Asn	Ser	Val	Leu	Met	Gly
		35					40					45			
Met	Lys	Asn	Gln	Leu	Ala	Val	Leu	Arg	Val	Ala	Gly	Ser	Leu	Gln	Lys
	50					55					60				
Ser	Thr	Glu	Val	Met	Lys	Ala	Met	Gln	Ser	Leu	Val	Lys	Ile	Pro	Glu
65					70					75					80
Ile	Gln	Ala	Thr	Met	Arg	Glu	Leu	Ser	Lys	Glu	Met	Met	Lys	Ala	Gly
				85					90					95	
Ile	Ile	Glu	Glu	Met	Leu	Glu	Asp	Thr	Phe	Glu	Ser	Met	Asp	Asp	Gln
			100					105					110		
Glu	Glu	Met	Glu	Glu	Glu	Ala	Glu	Met	Glu	Ile	Asp	Arg	Ile	Leu	Phe
		115					120					125			
Glu	Ile	Thr	Ala	Gly	Ala	Leu	Gly	Lys	Ala	Pro	Ser	Lys	Val	Thr	Asp
	130					135					140				
Ala	Leu	Pro	Glu	Pro	Glu	Pro	Pro	Gly	Ala	Met	Ala	Ala	Ser	Glu	Asp
145					150					155					160
Glu	Gly	Glu	Glu	Glu	Glu	Ala	Leu	Glu	Ala	Met	Gln	Ser	Arg	Leu	Ala
				165					170					175	
Thr	Leu	Arg	Ser												
			180												

&lt;210&gt; 237

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

Leu 1	Met	Pro	Phe	Gln 5	Ser	Gln	Asn	Leu	Gln 10	Glu	Arg	Trp	Leu	Pro 15	Gln
Arg	Met	Arg	Gly 20	Arg	Arg	Lys	Arg	Leu 25	Trp	Arg	Pro	Cys	Ser 30	Pro	Gly
Trp	Pro	His 35	Ser	Ala	Ala	Arg	Gly 40	Cys	Leu	Pro	Arg	Trp 45	Val	Cys	Thr
His	Ser 50	Ser	Gln	Glu	Leu	Pro 55	Phe	Tyr	Val	Ser	Leu 60	Ala	Leu	His	Leu
Cys 65	Cys	Glu	Asp	Tyr	His 70	Phe	Gly	Glu	Gly	Ser 75	Val	Cys	Leu	Phe	Ser 80
Phe	Ser	Ala	Gln	Val 85	Leu	Gly	Ser	Gln	Arg 90	Asp	Cys	Ser	Tyr	Lys 95	Ser
Gly	Ile	Asn	Lys 100	Cys	Ile	Ile	Phe	Arg 105	Lys	Lys	Lys	Lys	Lys 110	Lys	

&lt;210&gt; 238

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

Lys 1	Ile	Cys	Glu	Arg 5	Cys	Cys	Gln	Glu	Gly 10	Pro	Glu	Gly	Cys	Leu 15	His
Ser	Ser	Gly	Gln 20	Gly	Asp	Asp	Gln	Val 25	Lys	Glu	Gly	Cys	Glu 30	Gln	Ala
Val	Cys	Ile 35	Gln	Ser	Thr	His	Glu 40	Leu	Ser	Ala	His	Gly 45	Asp	Glu	Glu
Pro	Ala 50	Arg	Gly	Leu	Ala	Ser 55	Gly	Trp	Phe	Pro	Ala 60	Glu	Glu	His	Arg
Ser 65	Asp	Glu	Gly	His	Ala 70	Lys	Ser	Cys	Glu	Asp 75	Ser	Arg	Asp	Ser	Gly 80
His	His	Glu	Gly	Val 85	Val	Gln	Arg	Asn	Asp 90	Glu	Gly	Trp	Asp	His 95	Arg
Gly	Asp	Val	Arg 100	Gly	His	Phe									

&lt;210&gt; 239

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

Thr 1	Trp	Cys	Thr	Thr 5	Thr	Met	Leu	Ala	Ala 10	Arg	Leu	Val	Cys	Leu 15	Arg
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Thr	Leu	Pro	Ser 20	Arg	Val	Phe	His	Pro 25	Ala	Phe	Thr	Lys	Ala 30	Ser	Pro
Val	Val	Lys 35	Asn	Ser	Ile	Thr	Lys 40	Asn	Gln	Trp	Leu	Leu 45	Thr	Pro	Ser
Arg	Glu 50	Tyr	Ala	Thr	Lys	Thr 55	Arg	Ile	Gly	Ile	Arg 60	Arg	Gly	Arg	Thr
Gly 65	Gln	Glu	Leu	Lys	Glu 70	Ala	Ala	Leu	Glu	Pro 75	Ser	Met	Glu	Lys	Ile 80
Phe	Lys	Ile	Asp	Gln 85	Met	Gly	Arg	Trp	Phe 90	Val	Ala	Gly	Gly	Ala 95	Ala
Val	Gly	Leu	Gly 100	Ala	Leu	Cys	Tyr	Tyr 105	Gly	Leu	Gly	Leu	Ser 110	Asn	Glu
Ile	Gly	Ala 115	Ile	Glu	Lys	Ala	Val 120	Ile	Trp	Pro	Gln	Tyr 125	Val	Lys	Asp
Arg	Ile 130	His	Ser	Thr	Tyr	Met 135	Tyr	Leu	Ala	Gly	Ser 140	Ile	Gly	Leu	Thr
Ala 145	Leu	Ser	Ala	Ile	Ala 150	Ile	Ser	Arg	Thr	Pro 155	Val	Leu	Met	Asn	Phe 160
Met	Met	Arg	Gly	Ser 165	Trp	Val	Thr	Ile	Gly 170	Val	Thr	Phe	Ala	Ala 175	Met
Val	Gly	Ala	Gly 180	Met	Leu	Val	Arg	Ser 185	Ile	Pro	Tyr	Asp	Gln 190	Ser	Pro
Gly	Pro	Lys 195	His	Leu	Ala	Trp	Leu 200	Leu	His	Ser	Gly	Val 205	Met	Gly	Ala
Val	Val 210	Ala	Pro	Leu	Thr	Ile 215	Leu	Gly	Gly	Pro	Leu 220	Leu	Ile	Arg	Ala
Ala 225	Trp	Tyr	Thr	Ala	Gly 230	Ile	Val	Gly	Gly	Leu 235	Ser	Thr	Val	Ala	Met 240
Cys	Ala	Pro	Ser	Glu 245	Lys	Phe	Leu	Asn	Met 250	Gly	Ala	Pro	Leu	Gly 255	Val
Gly	Leu	Gly	Leu 260	Val	Phe	Val	Ser	Ser 265	Leu	Gly	Ser	Met	Phe 270	Leu	Pro
Pro	Thr	Thr 275	Val	Ala	Gly	Ala	Thr 280	Leu	Tyr	Ser	Val	Ala 285	Met	Tyr	Gly
Gly	Leu 290	Val	Leu	Phe	Ser	Met 295	Phe	Leu	Leu	Tyr	Asp 300	Thr	Gln	Lys	Val
Ile 305	Lys	Arg	Ala	Glu	Val 310	Ser	Pro	Met	Tyr	Gly 315	Val	Gln	Lys	Tyr	Asp 320
Pro	Ile	Asn	Ser	Met 325	Leu	Ser	Ile	Tyr	Met 330	Asp	Thr	Leu	Asn	Ile 335	Phe
Met	Arg	Val	Ala 340	Thr	Met	Leu	Ala	Thr 345	Gly	Gly	Asn	Arg	Lys 350	Lys	

<210> 240  
 <211> 147  
 <212> PRT  
 <213> Homo sapiens

<400> 240

Arg 1	Val	Ala	Pro	Ala 5	Thr	Val	Val	Gly	Gly 10	Arg	Asn	Ile	Asp	Pro 15	Asn
Glu	Asp	Thr	Lys 20	Thr	Arg	Pro	Arg	Pro 25	Thr	Pro	Arg	Gly	Ala 30	Pro	Met
Phe	Arg	Asn 35	Phe	Ser	Leu	Gly	Ala 40	His	Met	Ala	Thr	Val 45	Glu	Arg	Pro
Pro	Thr 50	Met	Pro	Ala	Val	Tyr 55	His	Ala	Ala	Leu	Met 60	Arg	Arg	Gly	Pro
Pro 65	Asn	Ile	Val	Arg	Gly 70	Ala	Thr	Thr	Ala	Pro 75	Ile	Thr	Pro	Glu	Cys 80
Ser	Asn	Gln	Ala	Arg 85	Cys	Phe	Gly	Pro	Gly 90	Leu	Trp	Ser	Tyr	Gly 95	Ile
Asp	Arg	Thr	Ser 100	Ile	Pro	Ala	Pro	Thr 105	Met	Ala	Ala	Lys	Val 110	Thr	Pro
Ile	Val	Thr 115	Gln	Glu	Pro	Leu	Ile 120	Met	Lys	Phe	Met	Arg 125	Thr	Gly	Val
Leu	Leu 130	Ile	Ala	Met	Ala	Asp 135	Lys	Ala	Val	Lys	Pro 140	Ile	Leu	Pro	Ala
Lys 145	Tyr	Ile													

<210> 241  
 <211> 196  
 <212> PRT  
 <213> Homo sapiens

<400> 241

Lys 1	Ala	Arg	Arg	Arg 5	Gly	Thr	Met	Ala	Ala 10	Ala	Ala	Asp	Glu	Arg 15	Ser
Pro	Glu	Asp	Gly 20	Glu	Asp	Glu	Glu	Glu 25	Glu	Glu	Gln	Leu	Val 30	Leu	Val
Glu	Leu	Ser 35	Gly	Ile	Ile	Asp	Ser 40	Asp	Phe	Leu	Ser	Lys 45	Cys	Glu	Asn
Lys 50	Cys	Lys	Val	Leu	Gly	Ile 55	Asp	Thr	Glu	Arg	Pro 60	Ile	Leu	Gln	Val
Asp 65	Ser	Cys	Val	Phe	Ala 70	Gly	Glu	Tyr	Glu	Asp 75	Thr	Leu	Gly	Thr	Cys 80
Val	Ile	Phe	Glu	Glu 85	Asn	Val	Glu	His	Ala 90	Asp	Thr	Glu	Gly	Asn 95	Asn
Lys	Thr	Val	Leu	Lys	Tyr	Lys	Cys	His	Thr	Met	Lys	Lys	Leu	Ser	Met

100							105					110				
Thr	Arg	Thr	Leu	Leu	Thr	Glu	Lys	Lys	Glu	Gly	Glu	Glu	Asn	Ile	Gly	
		115					120					125				
Gly	Val	Glu	Trp	Leu	Gln	Ile	Lys	Asp	Asn	Asp	Phe	Ser	Tyr	Arg	Pro	
	130					135					140					
Asn	Met	Ile	Cys	Asn	Phe	Leu	His	Glu	Asn	Glu	Asp	Glu	Glu	Val	Val	
145					150					155					160	
Ala	Ser	Ala	Pro	Asp	Lys	Ser	Leu	Glu	Leu	Glu	Glu	Glu	Glu	Ile	Gln	
				165					170					175		
Met	Asn	His	Arg	Phe	Lys	Pro	Gly	Phe	Val	Glu	Pro	Gly	Glu	Pro	Ile	
			180					185					190			
Ala	Pro	Trp	Glu													
			195													

&lt;210&gt; 242

&lt;211&gt; 156

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

Pro	Pro	Ala	Pro	Ala	Leu	Arg	His	Arg	Glu	Thr	Arg	Arg	Pro	Val	Ala
1				5					10					15	
Ser	Leu	His	Val	Gly	Thr	Gly	Ala	Leu	Gly	Ala	Arg	Ser	His	Pro	Pro
			20					25					30		
Ala	Gly	Ser	Arg	His	Leu	Glu	Phe	Trp	Gln	Lys	Gln	Phe	Ala	Arg	Arg
		35					40					45			
Gly	Ala	Asp	Gly	Gln	Glu	Pro	Asn	Lys	Leu	Leu	Arg	Leu	Gly	Ala	Glu
	50					55					60				
Ala	Arg	Thr	Gln	Asp	Gly	Gly	Ser	Gly	Arg	Ala	Trp	Pro	Val	Thr	Arg
	65				70					75					80
Arg	Arg	Gly	Ala	Ala	Gly	Pro	Trp	Arg	Arg	Arg	Arg	Thr	Ser	Gly	Val
				85					90					95	
Gln	Arg	Thr	Glu	Lys	Thr	Arg	Lys	Arg	Arg	Ser	Ser	Trp	Phe	Trp	Trp
			100					105					110		
Asn	Tyr	Gln	Glu	Leu	Leu	Ile	Gln	Thr	Ser	Ser	Gln	Asn	Val	Lys	Ile
		115					120					125			
Asn	Ala	Arg	Phe	Trp	Ala	Leu	Thr	Leu	Arg	Gly	Pro	Phe	Cys	Lys	Trp
	130					135					140				
Thr	Ala	Val	Ser	Leu	Leu	Gly	Ser	Met	Lys	Thr	Leu				
					150					155					

&lt;210&gt; 243

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

Arg 1	Arg	Leu	Glu	Val 5	Ser	Tyr	Arg	Gln	His 10	His	Phe	Arg	Val	Ser 15	Leu
Ala	Pro	Trp	Ser 20	Lys	Met	Ala	Asp	Glu 25	Ala	Thr	Arg	Arg	Val 30	Val	Ser
Glu	Ile	Pro 35	Val	Leu	Lys	Thr	Asn 40	Ala	Gly	Pro	Arg	Asp 45	Arg	Glu	Leu
Trp	Val 50	Gln	Arg	Leu	Lys	Glu 55	Glu	Tyr	Gln	Ser	Leu 60	Ile	Arg	Tyr	Val
Glu 65	Asn	Asn	Lys	Asn	Ala 70	Asp	Asn	Asp	Trp	Phe 75	Arg	Leu	Glu	Ser	Asn 80
Lys	Glu	Gly	Thr	Arg 85	Trp	Phe	Gly	Lys	Cys 90	Trp	Tyr	Ile	His	Asp 95	Leu
Leu	Lys	Tyr	Glu 100	Phe	Asp	Ile	Glu	Phe 105	Asp	Ile	Pro	Ile	Thr 110	Tyr	Pro
Thr	Thr	Ala 115	Pro	Glu	Ile	Ala	Val 120	Pro	Glu	Leu	Asp	Gly 125	Lys	Thr	Ala
Lys	Met 130	Tyr	Arg												

&lt;210&gt; 244

&lt;211&gt; 159

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

Leu 1	Phe	Ala	Ile	Ser 5	Tyr	Ser	Val	Leu	Pro 10	Val	His	Leu	Cys	Cys 15	Leu
Ser	Ile	Gln	Leu 20	Arg	Asn	Cys	Asn	Phe 25	Trp	Gly	Ser	Ser	Arg 30	Ile	Cys
Asp	Arg	Asn 35	Val	Lys	Leu	Asp	Val 40	Lys	Leu	Ile	Phe	Gln 45	Glu	Val	Met
Asp	Ile 50	Pro	Ala	Phe	Ser	Lys 55	Pro	Pro	Ser	Ser	Phe 60	Leu	Val	Gly	Leu
Gln 65	Ser	Glu	Pro	Ile	Val 70	Val	Ser	Ile	Leu	Val 75	Val	Leu	His	Ile	Pro 80
Asp	Lys	Gly	Leu	Ile 85	Phe	Leu	Leu	Gln	Ser 90	Leu	His	Pro	Gln	Leu 95	Thr
Ile	Ser	Gly	Ser 100	Gly	Val	Ser	Leu	Gln 105	His	Arg	Asp	Leu	Arg 110	His	Asn
Thr	Ser	Arg 115	Gly	Phe	Ile	Arg	His 120	Leu	Gly	Pro	Gly	Arg 125	Lys	Arg	Asn
Ala	Glu 130	Val	Val	Leu	Pro	Val 135	Ala	Tyr	Leu	Lys	Ala 140	Pro	Ser	Ser	Leu
Leu	Trp	Glu	Asp	Glu	Thr	Leu	Gly	Cys	Cys	Lys	Thr	Ser	Phe	Glu	



145  
 <210> 245  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

150

155

&lt;400&gt; 245

Ala 1	Thr	Leu	Pro	Asp 5	Ala	Leu	Pro	Pro	Ala 10	Thr	Lys	Phe	Phe	Leu 15	Lys
Ala	Phe	Phe	Asp 20	Ser	Leu	Pro	Ser	Pro 25	Ile	Gln	Ser	Tyr	Leu 30	Tyr	Ile
Phe	Ala	Val 35	Phe	Pro	Ser	Ser	Ser 40	Gly	Thr	Ala	Ile	Ser 45	Gly	Ala	Val
Val	Gly 50	Tyr	Val	Ile	Gly	Met 55	Ser	Asn	Ser	Met	Ser 60	Asn	Ser	Tyr	Phe
Arg 65	Arg	Ser	Trp	Ile	Tyr 70	Gln	His	Phe	Pro	Asn 75	His	Arg	Val	Pro	Ser 80
Leu	Leu	Asp	Ser	Ser 85	Arg	Asn	Gln	Ser	Leu 90	Ser	Ala	Phe	Leu	Leu 95	Phe
Ser	Thr	Tyr	Arg 100	Ile	Arg	Asp									

<210> 246  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 246

Ala 1	Val	Arg	Arg	Arg 5	Gly	Ala	Leu	Ser	Leu 10	Ser	Val	Gly	Ala	Ala 15	Cys
Gly	Leu	Val	Ala 20	Leu	Trp	Gln	Arg	Arg 25	Arg	Gln	Asp	Ser	Gly 30	Thr	Met
Ser	Gly	Phe 35	Ser	Thr	Glu	Glu	Arg 40	Ala	Ala	Pro	Phe	Ser 45	Leu	Glu	Tyr
Arg	Val 50	Phe	Leu	Lys	Asn	Glu 55	Lys	Gly	Gln	Tyr	Ile 60	Ser	Pro	Phe	His
Asp 65	Ile	Pro	Ile	Tyr	Ala 70	Asp	Lys	Asp	Val	Phe 75	His	Met	Val	Val	Glu 80
Val	Pro	Arg	Trp	Ser 85	Asn	Ala	Lys	Met	Glu 90	Ile	Ala	Thr	Lys	Asp 95	Pro
Leu	Asn	Pro	Ile 100	Lys	Gln	Asp	Val	Lys 105	Lys	Gly	Lys	Leu	Arg 110	Tyr	Val
Ala	Asn	Leu 115	Phe	Pro	Tyr	Lys	Gly 120	Tyr	Ile	Trp	Asn	Tyr 125	Gly	Ala	Ile
Pro	Gln 130	Thr	Trp	Glu	Asp	Pro 135	Gly	His	Asn	Asp	Lys 140	His	Thr	Gly	Cys

Cys 145	Gly	Asp	Asn	Asp	Pro 150	Ile	Asp	Val	Cys	Glu 155	Ile	Gly	Ser	Lys	Val 160
Cys	Ala	Arg	Gly	Glu 165	Ile	Ile	Gly	Val	Lys 170	Val	Leu	Gly	Ile	Leu 175	Ala
Met	Ile	Asp	Glu 180	Gly	Glu	Thr	Asp	Trp 185	Lys	Val	Ile	Ala	Ile 190	Asn	Val
Asp	Asp	Pro 195	Asp	Ala	Ala	Asn	Tyr 200	Asn	Asp	Ile	Asn	Asp 205	Val	Lys	Arg
Leu	Lys 210	Pro	Gly	Tyr	Leu	Glu 215	Ala	Thr	Val	Asp	Trp 220	Phe	Arg	Arg	Tyr
Lys 225	Val	Pro	Asp	Gly	Lys 230	Pro	Glu	Asn	Glu	Phe 235	Ala	Phe	Asn	Ala	Glu 240
Phe	Lys	Asp	Lys	Asp 245	Phe	Ala	Ile	Asp	Ile 250	Ile	Lys	Ser	Thr	His 255	Asp
His	Trp	Lys	Ala 260	Leu	Val	Thr	Lys	Lys 265	Thr	Asn	Gly	Lys	Arg 270	Ile	Met
Leu	Ile	Val 275	Gln	Leu	Phe	Val	Gly 280	Pro	Leu	Lys	Val	Cys 285			

<210> 247  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 247

Thr 1	Lys	Gly	Leu	Arg 5	Ile	Ala	Gln	Ala	Gln 10	Leu	Cys	Pro	Gly	Ser 15	Pro
Arg	Cys	Arg	Ser 20	Gln	Ser	Ile	Ser	Arg 25	Arg	Ala	Cys	Ala	Leu 30	Cys	Leu
Arg	Pro	Ser 35	Thr	Gln	Pro	Asn	Thr 40	Thr	Tyr	Leu	Arg	Lys 45	Pro	Gly	Gly
Arg	Lys 50	Arg	Ala	Val	Gly	His 55	Lys	Ser	Pro	Ala	Glu 60	Thr	Arg	Val	Pro
Ala 65	Ser	Val	Gln	Arg	Ser 70	Gln	Pro	Pro	Arg	Ala 75	His	Arg	Lys	Ser	Cys 80
Leu	Ala	Ser	Leu	Gly 85	Leu	Cys	Lys	Asn	Asn 90	Lys	Cys	Leu	Ser		

<210> 248  
 <211> 113  
 <212> PRT  
 <213> Homo sapiens

<400> 248

Asp 1	Pro	Arg	Pro	Ser 5	Arg	Ile	Gln	His	Ile 10	Ser	Gly	Asn	Pro	Ala 15	Gly
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Ala	Ser	Glu	Arg 20	Leu	Ala	Ile	Arg	Ala 25	Gln	Leu	Lys	Arg	Glu 30	Tyr	Leu
Leu	Gln	Tyr 35	Asn	Asp	Pro	Asn	Arg 40	Arg	Gly	Leu	Ile	Glu 45	Asn	Pro	Ala
Leu	Leu 50	Arg	Trp	Ala	Tyr	Ala 55	Arg	Thr	Ile	Asn	Val 60	Tyr	Pro	Asn	Phe
Arg 65	Pro	Thr	Pro	Lys	Asn 70	Ser	Leu	Met	Gly	Ala 75	Leu	Cys	Gly	Phe	Gly 80
Pro	Leu	Ile	Phe	Ile 85	Tyr	Tyr	Ile	Ile	Lys 90	Thr	Glu	Arg	Asp	Arg 95	Lys
Glu	Lys	Leu	Ile 100	Gln	Glu	Gly	Lys	Leu 105	Asp	Arg	Thr	Phe	His 110	Leu	Ser

Tyr

&lt;210&gt; 249

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 249

Val 1	Phe	Arg	Ser	Gly 5	Ser	Glu	Ile	Arg	Ile 10	Asp	Ile	Tyr	Cys	Ser 15	Cys
Ile	Gly	Pro	Thr 20	Lys	Gln	Gly	Arg	Ile 25	Phe	Asp	Glu	Pro	Ser 30	Ala	Val
Gly	Ile	Val 35	Val	Leu	Lys	Gln	Val 40	Leu	Ser	Phe	Gln	Leu 45	Gly	Ser	Tyr
Gly	Gln 50	Pro	Leu	Ala	Cys	Ala 55	Arg	Arg	Val	Ser	Gly 60	Asp	Met	Leu	Tyr
Ser 65	Ala	Gly	Ser	Arg	Val 70	Ser	Gly	Arg	Val	Arg 75	Arg	Leu	Asp	Gly	Leu 80
Tyr	Phe	Gly	Asn	Asp 85	Ile	Leu	Ala	Asn	Gln 90	Gly	Thr	Ile	Ala	Pro 95	Ala

Arg Phe

&lt;210&gt; 250

&lt;211&gt; 158

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

Thr 1	Gln	Val	Met	Val 5	Gln	Ser	Met	Phe	Ala 10	Pro	Thr	Asp	Thr	Ser 15	Asp
Met	Glu	Ala	Val 20	Trp	Lys	Glu	Ala	Lys 25	Pro	Glu	Asp	Leu	Met 30	Asp	Ser
Lys	Leu	Arg 35	Cys	Val	Phe	Glu	Leu 40	Pro	Ala	Glu	Asn	Asp 45	Lys	Pro	His

Asp	Val	Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu
	50					55					60				
Thr	Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
65					70					75					80
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val	Gln
				85					90					95	
Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly	Leu	Arg
			100					105					110		
Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala	Leu	Ala	Pro
		115					120					125			
Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu	Ala	Leu	Val	Val
	130					135					140				
Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys	Ile	Ala	Leu		
145					150					155					

&lt;210&gt; 251

&lt;211&gt; 112

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

Val	Asn	Lys	Ala	Leu	Pro	Phe	Ile	Ser	Lys	Ala	Leu	Gly	Gln	Ser	Val
1				5					10					15	
Asn	Thr	Arg	Leu	Ser	Leu	Met	Thr	Ser	Thr	Ser	Asp	Ala	Ala	Thr	Val
			20					25					30		
Gln	Phe	Leu	Trp	Ala	Ser	Asp	Ser	Val	His	Gln	Ser	Gln	Gly	Ala	Asp
		35					40					45			
Gly	Leu	Asp	Arg	Thr	Glu	Asp	Thr	Glu	Ser	Ser	Leu	Gly	Arg	Glu	Trp
	50					55					60				
Ala	Thr	Trp	Gly	Leu	Leu	Cys	Gly	Ala	Asp	Arg	Thr	Pro	Gln	His	Ala
65					70					75					80
Gly	Leu	Gln	Leu	Pro	Lys	Gly	Gln	His	Gln	Gln	Ala	Arg	Lys	Gly	Val
				85					90					95	
Ile	Leu	Arg	Glu	Val	Ile	Gln	His	His	Val	Pro	Arg	Pro	Thr	Asn	Val
			100					105					110		

&lt;210&gt; 252

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

Ser	Lys	Gly	Cys	Ser	Ile	Thr	Glu	Thr	Val	Thr	Val	Asp	Pro	Gly	Ser
1				5					10					15	
Ile	Ile	Pro	Leu	Leu	Gly	Leu	Thr	Gln	Tyr	Arg	Arg	Gly	Ala	Val	Val
			20					25					30		
Phe	Thr	Leu	Lys	His	Thr	Phe	Leu	Ser	Asp	Gly	Phe	Arg	Asn	Leu	Arg

35					40					45						
Phe	Val	Val	Thr	Thr	Ser	Val	Lys	Gly	Pro	Leu	Asn	Leu	Arg	Ser	Val	
	50					55					60					
Gly	Gly	Ser	Arg	Thr	Arg	Ile	Cys	Ser	Ser	Ser	Pro	Trp	Pro	Leu	Arg	
65					70					75					80	
Arg	Thr	Pro	Ser	Glu	Arg	Gln	Arg	Arg	Ala	Gly	Gly	Gly	Leu	Leu	Ala	
				85					90					95		
Gly	Gly	Gly	Gly	Arg	Trp	Arg	Glu	Gly	Arg	Gly	Ser	Glu	Phe	Ala	Ser	
			100					105					110			
Leu	Leu	Phe	Leu	Val	Arg	Leu	Cys	Ser	Thr	Thr	Phe	Leu	Cys	Trp	Gln	
		115					120					125				
Ile	Cys	Phe	Gln	Ile	Asp	Phe										
	130					135										
<210> 253																
<211> 189																
<212> PRT																
<213> Homo sapiens																
<400> 253																
Ser	Met	Gln	Ser	Ala	Val	Ser	Phe	Phe	Phe	Phe	Ser	Leu	Asp	Gln	Lys	
1				5					10					15		
Lys	Ile	Cys	Leu	Pro	Thr	Ile	Ser	Leu	Val	Val	Trp	Pro	Thr	Val	Thr	
			20					25					30			
Ile	Phe	Leu	Cys	Val	Gln	Arg	His	Ile	Gly	Phe	Ala	Phe	Asn	Asp	Leu	
		35					40					45				
Leu	Arg	Leu	Glu	Asn	Thr	Ile	Lys	Thr	Asn	Cys	Ser	Ala	Thr	Gly	Gln	
	50					55					60					
Val	Val	Tyr	Tyr	Gln	Ile	Ile	Thr	Ser	Arg	Cys	Gln	Leu	His	Ile	Glu	
65					70					75					80	
Ser	Phe	Met	Lys	Phe	Ile	Asn	Lys	Glu	Leu	Phe	Phe	Leu	Cys	Gly	Phe	
				85					90					95		
Asn	Lys	Ser	Ser	Arg	Ile	Val	Gln	Ser	Leu	Val	Asn	Val	Ile	Leu	Ile	
			100					105					110			
Ile	Pro	Leu	Asn	Phe	Ile	Cys	Cys	Cys	Tyr	Leu	Leu	Lys	Tyr	Asp	Leu	
		115					120					125				
Phe	Arg	Leu	Leu	Ile	Pro	Leu	Ile	Gln	Glu	Met	Pro	Arg	Gly	Ile	Pro	
	130					135					140					
Trp	Gly	Asn	Gly	Ala	Ser	Tyr	Ser	Val	Asn	Phe	Ser	Ser	Phe	Thr	Phe	
145					150					155					160	
Ala	Asn	Ile	Met	Ala	Glu	Phe	Phe	Leu	Ser	Leu	Val	Arg	Gln	Leu	Leu	
				165					170					175		
Thr	Glu	Phe	Phe	Ile	Leu	Thr	Ile	Leu	Ser	His	Gly	Ile				
			180					185								

<210> 254  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 254

Lys 1	Ser	Ile	Trp	Lys 5	Gln	Ile	Cys	Gln	His 10	Lys	Asn	Val	Val	Glu 15	Gln
Ser	Leu	Thr	Arg 20	Lys	Arg	Arg	Asp	Ala 25	Asn	Ser	Leu	Pro	Leu 30	Pro	Ser
Arg	His	Arg 35	Pro	Pro	Pro	Pro	Ala 40	Ser	Lys	Pro	Pro	Pro 45	Ala	Leu	Arg
Cys	Leu 50	Ser	Asp	Gly	Val	Arg 55	Leu	Arg	Gly	His	Gly 60	Glu	Asp	Glu	Gln
Ile 65	Leu	Val	Leu	Asp	Pro 70	Pro	Thr	Asp	Leu	Lys 75	Phe	Lys	Gly	Pro	Phe 80
Thr	Asp	Val	Val	Thr 85	Thr	Asn	Leu	Lys	Leu 90	Arg	Asn	Pro	Ser	Asp 95	Arg
Lys	Val	Cys	Phe 100	Lys	Val	Lys	Thr	Thr 105	Ala	Pro	Arg	Arg	Tyr 110	Cys	Val
Arg	Pro	Asn 115	Ser	Gly	Ile	Ile	Asp 120	Pro	Gly	Ser	Thr	Val 125	Thr	Val	Ser
Val	Met 130	Leu	Gln	Pro	Phe	Asp 135	Tyr	Asp	Pro	Asn	Glu 140	Lys	Ser	Lys	His
Lys 145	Phe	Met	Val	Gln	Thr 150	Ile	Phe	Ala	Pro	Pro 155	Asn	Thr	Ser	Asp	Met 160
Glu	Ala	Val	Trp	Lys 165	Glu	Ala	Lys	Pro	Asp 170	Glu	Leu	Met	Asp	Ser 175	Lys
Leu	Arg	Cys	Val 180	Phe	Glu	Met	Pro	Asn 185	Glu	Asn	Asp	Lys	Leu 190	Asn	Asp
Met	Glu	Pro 195	Ser	Lys	Ala	Val	Pro 200	Leu	Asn	Ala	Ser	Lys 205	Gln	Asp	Gly
Pro	Met 210	Pro	Lys	Pro	His	Ser 215	Val	Ser	Leu	Asn	Asp 220	Thr	Glu	Thr	Arg
Lys 225	Leu	Met	Glu	Glu	Cys 230	Lys	Arg	Leu	Gln	Gly 235	Glu	Met	Met	Lys	Leu 240
Ser	Glu	Glu	Asn	Arg 245	His	Leu	Arg	Asp	Glu 250	Gly	Leu	Arg	Leu	Arg 255	Lys
Val	Ala	His	Ser 260	Asp	Lys	Pro	Gly	Ser 265	Thr	Ser	Thr	Ala	Ser 270	Phe	Arg
Asp	Asn	Val 275	Thr	Ser	Pro	Leu	Pro 280	Ser	Leu	Leu	Val	Val 285	Ile	Ala	Ala
Ile	Phe 290	Ile	Gly	Phe	Phe	Leu 295	Gly	Lys	Phe	Ile	Leu 300				

<210> 255  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 255

Gly 1	Ser	Ser	Gly	Ser 5	Arg	Phe	Glu	Val	Val 10	Val	Val	Leu	Glu	Glu 15	Arg
Arg	Gly	Gly	Arg 20	Gly	Arg	Gly	Met	Gly 25	Arg	Gly	Asp	Gly	Phe 30	Asp	Ser
Arg	Gly	Lys 35	Arg	Glu	Phe	Asp	Arg 40	His	Ser	Gly	Ser	Asp 45	Arg	Ser	Gly
Leu	Lys 50	His	Glu	Asp	Lys	Arg 55	Gly	Gly	Ser	Gly	Ser 60	His	Asn	Trp	Gly
Thr 65	Val	Lys	Asp	Glu	Leu 70	Thr	Glu	Ser	Pro	Lys 75	Tyr	Ile	Gln	Lys	Gln 80
Ile	Ser	Tyr	Asn	Tyr 85	Ser	Asp	Leu	Asp	Gln 90	Ser	Asn	Val	Thr	Glu 95	Glu
Thr	Pro	Glu	Gly 100	Glu	Glu	His	His	Pro 105	Val	Ala	Asp	Thr	Glu 110	Asn	Lys
Glu	Asn	Glu 115	Val	Glu	Glu	Val	Lys 120	Glu	Glu	Gly	Pro	Lys 125	Glu	Met	Thr
Leu	Asp 130	Glu	Trp	Lys	Ala	Ile 135	Gln	Asn	Lys	Asp	Arg 140	Ala	Lys	Val	Glu
Phe 145	Asn	Ile	Arg	Lys	Pro 150	Asn	Glu	Gly	Ala	Asp 155	Gly	Gln	Trp	Lys	Lys 160
Gly	Phe	Val	Leu	His 165	Lys	Ser	Lys	Ser	Glu 170	Glu	Ala	His	Ala	Glu 175	Asp
Ser	Val	Met	Asp 180	His	His	Phe	Arg	Lys 185	Pro	Ala	Asn	Asp	Ile 190	Thr	Ser
Gln	Leu	Glu 195	Ile	Asn	Phe	Gly	Asp 200	Leu	Gly	Arg	Pro	Gly 205	Arg	Gly	Gly
Arg	Gly 210	Gly	Arg	Gly	Gly	Arg 215	Gly	Arg	Gly	Gly	Arg 220	Pro	Asn	Arg	Gly
Ser 225	Arg	Thr	Asp	Lys	Ser 230	Ser	Ala	Ser	Ala	Pro 235	Asp	Val	Asp	Asp	Pro 240
Glu	Ala	Phe	Pro	Ala 245	Leu	Ala									

<210> 256  
 <211> 69  
 <212> PRT  
 <213> Homo sapiens

<400> 256

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Val	Leu	Val	Leu 20	Gln	Ala	Arg	Ser	Ile 25	Thr	Ser	Thr	Met	Pro 30	Ile	Lys
Phe	Thr	Phe 35	Ala	Thr	Arg	Ile	Lys 40	Ser	Ile	Ser	Ser	Ala 45	His	Ser	Thr
Ser	Thr 50	Ala	Pro	Ser	Thr	Leu 55	Phe	Gln	Asp	His	His 60	Asp	Leu	Glu	Ser
Arg 65	Ala	Ala	Arg	Ala											

&lt;210&gt; 257

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 257

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Tyr	Asp	Gly	Gly 20	Tyr	Gly	Gly	Phe	Asp 25	Asp	Tyr	Gly	Gly	Tyr 30	Asn	Asn
Tyr	Gly	Tyr 35	Gly	Asn	Asp	Gly	Phe 40	Asp	Asp	Arg	Met	Arg 45	Asp	Gly	Arg
Gly	Met 50	Gly	Gly	His	Gly	Tyr 55	Gly	Gly	Ala	Gly	Asp 60	Ala	Ser	Ser	Gly
Phe 65	His	Gly	Gly	His	Phe 70	Val	His	Met	Arg	Gly 75	Leu	Pro	Phe	Arg	Ala 80
Thr	Glu	Asn	Asp	Ile 85	Ala	Asn	Phe	Phe	Ser 90	Pro	Leu	Asn	Pro	Ile 95	Arg
Val	His	Ile	Asp 100	Ile	Gly	Ala	Asp	Gly 105	Arg	Ala	Thr	Gly	Glu 110	Ala	Asp
Val	Glu	Phe 115	Val	Thr	His	Glu	Asp 120	Ala	Val	Ala	Ala	Met 125	Ser	Lys	Asp
Lys	Asn 130	Asn	Met	Gln	His	Arg 135	Tyr	Ile	Glu	Leu	Phe 140	Leu	Asn	Ser	Thr
Pro 145	Gly	Gly	Gly	Ser	Gly 150	Met	Gly	Gly	Ser	Gly 155	Met	Gly	Gly	Tyr	Gly 160
Arg	Asp	Gly	Met	Asp 165	Asn	Gln	Gly	Gly	Tyr 170	Gly	Ser	Val	Gly	Arg 175	Met
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<210> 258  
 <211> 1105  
 <212> DNA  
 <213> Homo sapiens

<400> 258

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1105

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<210> 259  
 <211> 1088  
 <212> DNA  
 <213> Homo sapiens

<400> 259

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1088

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<210> 260  
 <211> 3292  
 <212> DNA  
 <213> Homo sapiens

<400> 260

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&lt;210&gt; 261

&lt;211&gt; 1196

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 261

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<210> 262

<211> 1467

<212> DNA

<213> Homo sapiens

<400> 262

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1467

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<210> 263

<211> 739

<212> DNA

<213> Homo sapiens

<400> 263

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739

&lt;210&gt; 264

&lt;211&gt; 2146

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 264

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2146

&lt;210&gt; 265

&lt;211&gt; 1020

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 265

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<210> 266

<211> 1652

<212> DNA

<213> Homo sapiens

<400> 266

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nccgggnntc ctgccttctg tccctgctcc tggccgngt ttgttccgcc gggccgggga 180
caagagaagt ctaagacaga ctgccatggc ggtnatgagt ggtaccatct acgagtatgg 240
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<210> 267

<211> 1409

<212> DNA

<213> Homo sapiens

<400> 267

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accctcgatt ggtttttccct gccatttaga tgttgaagta ccccatgaag agctgcaaaa 180

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tctgggttcat cctatgtaca gaatggcaca gggaatgcat atgaagagga agccaacaag 420
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ttgtatccac accattacat ttttttttaa attggagcca tctatgagcc tgatttgggt 1320
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1409

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<210> 268

<211> 900

<212> DNA

<213> Homo sapiens

<400> 268

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ctccggcctg ccagtgaagt tctaccatca tggacctatt gttcgggcgc cggaagacgc 180
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<210> 269

<211> 1145

<212> DNA

<213> Homo sapiens

<400> 269

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aagaactggg caatgagtgg tcatgaaga taagaaagga aatgagagtt gttgacaggc 180
aaataaggga tatccaaaga gaagaagaaa aagtgaacg atctgtgaaa gttgacaggc 240
agaagggcca gaaggatgtc tgcatagttc tggccaagga gatgatcagg tcaaggaagg 300
ctgtgagcaa gctgtatgca tccaaagcac acatgaactc agtgctcatg gggatgaaga 360
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ccatgcaaaag tcttgtaag attccagaga ttcaggccac catgaggagg ttgtccaaag 480
aaatgatgaa ggctgggatc atagaggaga tgtagagga cacttttgaa agcatggacg 540
atcaggaaga aatggaggaa gaagcagaaa tggaaattga cagaattctc tttgaaatta 600
cagcaggggc cttgggcaaa gcaaccagta aagtgactga tgcccttcca gagccagaac 660

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1145

```

<210> 270

<211> 1836

<212> DNA

<213> Homo sapiens

<400> 270

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ctggtgcacc accaccatgt tggtgcaag gctggtgtgt ctccggacac taccttctag 180
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1836

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<210> 271

<211> 1220

<212> DNA

<213> Homo sapiens

<400> 271

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atataggacg gagtaatctg tttacattct gttcttctcg atgcactcac aagcgggtaa 180
ctaggtgaca agaaaaaaaa gatcttattc aaaagaggct ttacagcaac ccaacgtctc 240
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gtttctcttg cgccctgggc caagatggcg gatgaagcca cgcgacgtgt tgtgtctgag 360
atccccggtg tgaagactaa cgccggaccc cgagatcggt agttgtgggt gcagcgactg 420

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aaaaaaaaaa aaaaaaaaaa
1220

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&lt;210&gt; 272

&lt;211&gt; 1303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

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1303

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&lt;210&gt; 273

&lt;211&gt; 1586

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

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cgggccag 1568

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&lt;210&gt; 274

&lt;211&gt; 144

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

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Tyr	Cys	Ala	Ile 20	Asp	Ser	Cys	Ile	Lys 25	Phe	Trp	Asn	Ala	Gly 30	Ser	Ser
Trp	Leu	Ser 35	Ser	Val	Thr	Leu	Trp 40	Ser	Met	Ser	Ser	Val 45	Ser	Leu	Ser
Ala	Ser 50	Asn	Val	Gly	Arg	Val 55	Arg	Ile	Lys	Ser	Glu 60	Gly	Cys	Ser	Thr
Gly 65	Asp	Lys	Leu	Ser	Leu 70	Gly	Val	Pro	Ala	Ser 75	Lys	Ala	Thr	Glu	Pro 80
Ile	Ser	Phe	Arg	Arg 85	Arg	Ser	Ser	Cys	Ser 90	Leu	Cys	Cys	Trp	Leu 95	Ser
Ala	Leu	Ala	Ser 100	Asp	Phe	Phe	Arg	Arg 105	Ser	Tyr	Ser	Gly	Arg 110	Tyr	Ser
Leu	Ser	Tyr 115	Ser	Ser	Ala	Ala	Leu 120	Val	Thr	Cys	Thr	Lys 125	Ser	Ser	Ser
Asn	Pro 130	Val	Pro	Arg	Thr	Ala 135	Glu	Thr	Pro	Thr	Thr 140	Leu	Ser	Glu	Leu

&lt;210&gt; 275

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 275

Met 1	Ser	Leu	Val	Leu 5	Asp	Glu	Phe	Tyr	Ser 10	Ser	Leu	Arg	Val	Val 15	Gly
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<210> 276
<211> 181
<212> PRT
<213> Homo sapiens
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[illegible]

180

<210> 277  
 <211> 89  
 <212> PRT  
 <213> Homo sapiens

<400> 277

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Thr	Ala	Ser 35	Ala	Leu	Cys	Ser	Arg 40	Trp	Leu	Gln	Arg	Cys 45	Arg	Asp	Val
Gly	Arg 50	Cys	Leu	Leu	Gln	Val 55	Gly	Gln	Gly	Ala	Leu 60	Arg	Asp	Val	Gly
Gly 65	Leu	Phe	Val	Leu	His 70	Val	Asp	Val	Leu	Gln 75	His	Leu	Leu	Pro	Met 80
Pro	Gln	Leu	Cys	Gln 85	Val	Leu	Leu	Asp							

<210> 278  
 <211> 401  
 <212> PRT  
 <213> Homo sapiens

<400> 278

Met 1	Pro	Asn	Phe	Cys 5	Ala	Ala	Pro	Asn	Cys 10	Thr	Arg	Lys	Ser	Thr 15	Gln
Ser	Asp	Leu	Ala 20	Phe	Phe	Arg	Phe	Pro 25	Arg	Asp	Pro	Ala	Arg 30	Cys	Gln
Lys	Trp	Val 35	Glu	Asn	Cys	Arg	Arg 40	Ala	Asp	Leu	Glu	Asp 45	Lys	Thr	Pro
Asp	Gln 50	Leu	Asn	Lys	His	Tyr 55	Arg	Leu	Cys	Ala	Lys 60	His	Phe	Glu	Thr
Ser 65	Met	Ile	Cys	Arg	Thr 70	Ser	Pro	Tyr	Arg	Thr 75	Val	Leu	Arg	Asp	Asn 80
Ala	Ile	Pro	Thr	Ile 85	Phe	Asp	Leu	Thr	Ser 90	His	Leu	Asn	Asn	Pro 95	His
Ser	Arg	His	Arg 100	Lys	Arg	Ile	Lys	Glu 105	Leu	Ser	Glu	Asp	Glu 110	Ile	Arg
Thr	Leu	Lys 115	Gln	Lys	Lys	Ile	Asp 120	Glu	Thr	Ser	Glu	Gln 125	Glu	Gln	Lys
His	Lys 130	Glu	Thr	Asn	Asn	Ser 135	Asn	Ala	Gln	Asn	Pro 140	Ser	Glu	Glu	Glu
Gly 145	Glu	Gly	Gln	Asp	Glu 150	Asp	Ile	Leu	Pro	Leu 155	Thr	Leu	Glu	Glu	Lys 160

Glu	Asn	Lys	Glu	Tyr 165	Leu	Lys	Ser	Leu	Phe 170	Glu	Ile	Leu	Ile	Leu 175	Met
Gly	Lys	Gln	Asn 180	Ile	Pro	Leu	Asp	Gly 185	His	Glu	Ala	Asp	Glu 190	Ile	Pro
Glu	Gly	Leu 195	Phe	Thr	Pro	Asp	Asn 200	Phe	Gln	Ala	Leu	Leu 205	Glu	Cys	Arg
Ile	Asn 210	Ser	Gly	Glu	Glu	Val 215	Leu	Arg	Lys	Arg	Phe 220	Glu	Thr	Thr	Ala
Val 225	Asn	Thr	Leu	Phe	Cys 230	Ser	Lys	Thr	Gln	Gln 235	Arg	Gln	Met	Leu	Glu 240
Ile	Cys	Glu	Ser	Cys 245	Ile	Arg	Glu	Glu	Thr 250	Leu	Arg	Glu	Val	Arg 255	Asp
Ser	His	Phe	Phe 260	Ser	Ile	Ile	Thr	Asp 265	Asp	Val	Val	Asp	Ile 270	Ala	Gly
Glu	Glu	His 275	Leu	Pro	Val	Leu	Val 280	Arg	Phe	Val	Asp	Glu 285	Ser	His	Asn
Leu	Arg 290	Glu	Glu	Phe	Ile	Gly 295	Phe	Leu	Pro	Tyr	Glu 300	Ala	Asp	Ala	Glu
Ile 305	Leu	Ala	Val	Lys	Phe 310	His	Thr	Met	Ile	Thr 315	Glu	Lys	Trp	Gly	Leu 320
Asn	Met	Glu	Tyr	Cys 325	Arg	Gly	Gln	Ala	Tyr 330	Ile	Val	Ser	Ser	Gly 335	Phe
Ser	Ser	Lys	Met 340	Lys	Val	Val	Ala	Ser 345	Arg	Leu	Leu	Glu	Lys 350	Tyr	Pro
Gln	Ala	Ile 355	Tyr	Thr	Leu	Cys	Ser 360	Ser	Cys	Ala	Leu	Asn 365	Met	Trp	Leu
Ala	Lys 370	Ser	Val	Pro	Val	Met 375	Gly	Val	Ser	Val	Ala 380	Leu	Gly	Thr	Ile
Glu 385	Glu	Val	Cys	Ser	Phe 390	Phe	His	Xxx	Ile	Thr 395	Thr	Thr	Ala	Phe	Arg 400

Thr

&lt;210&gt; 279

&lt;211&gt; 106

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 279

Met 1	Leu	Ile	Ser	Gly 5	Thr	Leu	Ser	His	Gly 10	Thr	Thr	Gln	Ile	Gln 15	Tyr
Xxx	Xxx	Glu	Glu 20	His	His	Ala	Asp	Met 25	Tyr	Arg	Ser	Asp	Leu 30	Pro	Asn
Pro	Asp	Thr 35	Leu	Ser	Ala	Glu	Leu 40	His	Cys	Trp	Arg	Ile 45	Lys	Trp	Lys

His	Arg	Gly	Lys	Asp	Ile	Glu	Leu	Pro	Ser	Thr	Ile	Tyr	Glu	Ala	Leu
	50					55					60				
His	Leu	Pro	Asp	Ile	Lys	Phe	Phe	Pro	Asn	Val	Tyr	Ala	Leu	Leu	Lys
65					70					75					80
Val	Leu	Cys	Ile	Leu	Pro	Val	Met	Lys	Val	Glu	Asn	Glu	Arg	Tyr	Glu
				85					90					95	
Asn	Gly	Thr	Lys	Ala	Ser	Leu	Lys	His	Ile						
			100					105							

<210> 280  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 280

Gly	Arg	Lys	Cys	Asn	Lys	Phe	Trp	Asp	Asn	Ala	Gln	Thr	Ser	Gly	Ile
1				5					10					15	
Glu	Glu	Pro	Ser	Glu	Thr	Lys	Gly	Ser	Met	Gln	Lys	Ser	Lys	Phe	Lys
			20					25					30		
Tyr	Lys	Leu	Val	Pro	Glu	Glu	Glu	Thr	Thr	Ala	Ser	Glu	Asn	Thr	Glu
		35					40					45			
Ile	Thr	Ser	Glu	Arg	Gln	Lys	Glu	Gly	Ile	Lys	Leu	Thr	Ile	Arg	Ile
	50					55					60				
Ser	Ser	Arg	Lys	Lys	Lys	Pro	Asp	Ser	Pro	Pro	Lys	Val	Leu	Glu	Pro
65				70						75					80
Glu	Asn	Lys	Gln	Glu	Lys	Thr	Glu	Lys	Glu	Glu	Glu	Lys	Thr	Asn	Val
				85					90					95	
Gly	Arg	Thr	Leu	Arg	Arg	Ser	Pro	Arg	Ile	Ser	Arg	Pro	Thr	Ala	Lys
			100					105					110		
Val	Ala	Glu	Ile	Arg	Asp	Gln	Lys	Ala	Asp	Lys	Lys	Arg	Gly	Glu	Gly
		115					120					125			
Glu	Asp	Glu	Val	Glu	Glu	Glu	Ser	Thr	Ala	Leu	Gln	Lys	Thr	Asp	Lys
	130					135					140				
Lys	Glu	Ile	Leu	Lys	Lys	Ser	Glu	Lys	Asp	Thr	Asn	Ser	Lys	Val	Ser
145				150						155					160
Lys	Val	Lys	Pro	Lys	Gly	Lys	Val	Arg	Trp	Thr	Gly	Ser	Arg	Thr	Arg
				165					170					175	
Gly	Arg	Trp	Lys	Tyr	Ser	Ser	Asn	Asp	Glu	Ser	Glu	Gly	Ser	Gly	Ser
			180					185					190		
Glu	Lys	Ser	Ser	Ala	Ala	Ser	Glu	Glu	Glu	Glu	Glu	Lys	Glu	Ser	Glu
		195					200					205			
Glu	Ala	Ile	Leu	Ala	Asp	Asp	Asp	Glu	Pro	Cys	Lys	Lys	Cys	Gly	Leu
	210				215						220				
Pro	Asn	His	Pro	Glu	Leu	Ile	Leu	Leu	Cys	Asp	Ser	Cys	Asp	Ser	Gly

225	230							235					240		
Tyr	His	Thr	Ala	Cys 245	Leu	Arg	Pro	Pro	Leu 250	Met	Ile	Ile	Pro	Asp 255	Gly
Glu	Trp	Phe	Cys 260	Pro	Pro	Cys	Gln	His 265	Lys	Leu	Leu	Cys	Glu 270	Lys	Leu
Glu	Glu	Gln 275	Leu	Gln	Asp	Leu	Asp 280	Val	Ala	Leu	Lys	Lys 285	Lys	Glu	Arg
Ala	Glu 290	Arg	Arg	Lys	Glu	Arg 295	Leu	Val	Tyr	Val	Gly 300	Ile	Ser	Ile	Glu
Asn 305	Ile	Ile	Pro	Pro	Gln 310	Glu	Pro	Asp	Phe	Ser 315	Glu	Asp	Gln	Glu	Glu 320
Lys	Lys	Lys	Asp	Ser 325	Lys	Lys	Ser	Lys	Ala 330	Asn	Leu	Leu	Glu	Arg 335	Arg
Ser	Thr	Arg	Thr 340	Arg	Lys	Cys	Ile	Ser 345	Tyr	Arg	Phe	Asp	Glu 350	Phe	Asp
Glu	Ala	Ile 355	Asp	Glu	Ala	Ile	Glu 360	Asp	Asp	Ile	Lys	Glu 365	Ala	Asp	Gly
Gly	Gly 370	Val	Gly	Arg	Gly	Lys 375	Asp	Ile	Ser	Thr	Ile 380	Thr	Gly	His	Arg
Gly 385	Lys	Asp	Ile	Ser	Thr 390	Ile	Leu	Asp	Glu	Lys 395	Ile	Ile	Thr		
<210> 281															
<211> 198															
<212> PRT															
<213> Homo sapiens															
<400> 281															
Ser 1	Ser	Glu	Lys	Ser 5	Gly	Ser	Cys	Gly	Gly 10	Met	Met	Phe	Ser	Ile 15	Leu
Ile	Pro	Thr	Tyr 20	Thr	Lys	Arg	Ser	Phe 25	Leu	Arg	Ser	Ala	Arg 30	Ser	Phe
Phe	Phe	Lys 35	Ala	Thr	Ser	Lys	Ser 40	Cys	Asn	Cys	Ser	Ser 45	Asn	Phe	Ser
Gln	Ser 50	Ser	Leu	Cys	Trp	Gln 55	Gly	Gly	Gln	Asn	His 60	Ser	Pro	Ser	Gly
Met 65	Ile	Ile	Arg	Gly	Gly 70	Arg	Arg	Gln	Ala	Val 75	Trp	Tyr	Pro	Leu	Ser 80
Gln	Glu	Ser	His	Arg 85	Arg	Ile	Ser	Ser	Gly 90	Trp	Phe	Gly	Arg	Pro 95	His
Phe	Leu	His	Gly 100	Ser	Ser	Ser	Ser	Ala 105	Arg	Met	Ala	Ser	Ser 110	Leu	Ser
Phe	Ser	Ser 115	Ser	Ser	Ser	Glu	Ala 120	Ala	Asp	Asp	Phe	Ser 125	Leu	Pro	Asp

Pro	Ser	Leu	Ser	Ser	Leu	Leu	Glu	Tyr	Phe	His	Leu	Pro	Arg	Val	Arg
	130					135					140				
Glu	Pro	Val	His	Arg	Thr	Leu	Pro	Leu	Gly	Phe	Thr	Leu	Leu	Thr	Leu
145					150					155					160
Glu	Phe	Val	Ser	Phe	Ser	Asp	Phe	Phe	Lys	Ile	Ser	Phe	Leu	Ser	Val
				165					170					175	
Phe	Cys	Lys	Ala	Val	Asp	Ser	Ser	Ser	Thr	Ser	Ser	Ser	Pro	Ser	Pro
			180					185					190		
Leu	Phe	Leu	Ser	Ala	Phe										
		195													

&lt;210&gt; 282

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

Gly	Arg	Leu	Pro	Phe	Ser	Gly	Arg	Gly	Arg	Gly	Lys	Lys	Val	Thr	Ser
1				5					10					15	
Gly	Asp	Gly	Val	Ala	Ser	Leu	Pro	Leu	Lys	Leu	Gly	Arg	Leu	Phe	Gly
			20					25					30		
Gly	Val	Thr	Arg	Gly	Phe	Asn	Met	Arg	Ile	Glu	Lys	Cys	Tyr	Phe	Cys
		35					40					45			
Ser	Gly	Pro	Ile	Tyr	Pro	Gly	His	Gly	Met	Met	Phe	Val	Arg	Asn	Asp
	50					55					60				
Cys	Lys	Val	Phe	Arg	Phe	Cys	Lys	Ser	Lys	Cys	His	Lys	Asn	Phe	Lys
65					70					75					80
Lys	Lys	Arg	Asn	Pro	Arg	Lys	Val	Arg	Trp	Thr	Lys	Ala	Phe	Arg	Lys
				85					90					95	
Ala	Ala	Gly	Lys	Glu	Leu	Thr	Val	Asp	Asn	Ser	Phe	Glu	Phe	Glu	Lys
			100					105					110		
Arg	Arg	Asn	Glu	Pro	Ile	Lys	Tyr	Gln	Arg	Glu	Leu	Trp	Asn	Lys	Thr
		115					120					125			
Ile	Asp	Ala	Met	Lys	Arg	Val	Glu	Glu	Ile	Lys	Gln	Lys	Arg	Gln	Ala
	130					135					140				
Lys	Phe	Ile	Met	Asn	Arg	Leu	Lys	Lys	Asn	Lys	Glu	Leu	Gln	Lys	Val
145					150					155					160
Gln	Asp	Ile	Lys	Glu	Val	Lys	Gln	Asn	Ile	His	Leu	Ile	Arg	Ala	Pro
				165					170					175	
Leu	Ala	Gly	Lys	Gly	Lys	Gln	Leu	Glu	Glu	Lys	Met	Val	Gln	Gln	Leu
			180					185					190		
Gln	Glu	Asp	Val	Asp	Met	Glu	Asp	Ala	Pro						
		195					200								

&lt;210&gt; 283

&lt;211&gt; 84

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 283

Ile 1	Ile	His	Cys	Lys 5	Leu	Phe	Thr	Ser	Cys 10	Phe	Pro	Glu	Cys	Phe 15	Gly
Pro	Pro	Asn	Phe 20	Ala	Arg	Ile	Ala	Leu 25	Leu	Phe	Lys	Val	Phe 30	Met	Thr
Phe	Arg	Phe 35	Ala	Lys	Ser	Glu	His 40	Leu	Ala	Ile	Val	Ala 45	Asp	Glu	His
His	Ala 50	Val	Ser	Arg	Ile	Asp 55	Gly	Pro	Arg	Thr	Glu 60	Ile	Thr	Leu	Phe
Asp 65	Thr	His	Val	Glu	Pro 70	Ala	Cys	Asn	Pro	Thr 75	Lys	Gln	Thr	Pro	Lys 80
Leu	Glu	Arg	Lys												

&lt;210&gt; 284

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 284

Arg 1	Leu	Glu	Pro	Arg 5	Ser	Val	Thr	Arg	Ser 10	Arg	Arg	Ala	Val	Ser 15	Arg
Leu	Ser	Ala	Arg 20	Pro	Gly	Lys	Val	Ser 25	Ala	Val	Met	Ala	Phe 30	Leu	Ala
Ser	Gly	Pro 35	Tyr	Leu	Thr	His	Gln 40	Gln	Lys	Val	Leu	Arg 45	Leu	Tyr	Lys
Arg	Ala 50	Leu	Arg	His	Leu	Glu 55	Ser	Trp	Cys	Val	Gln 60	Arg	Asp	Lys	Tyr
Arg 65	Tyr	Phe	Ala	Cys	Leu 70	Met	Arg	Ala	Arg	Phe 75	Glu	Glu	His	Lys	Asn 80
Glu	Lys	Asp	Met	Ala 85	Lys	Ala	Thr	Gln	Leu 90	Leu	Lys	Glu	Ala	Glu 95	Glu
Glu	Phe	Trp	Tyr 100	Arg	Gln	His	Pro	Gln 105	Pro	Tyr	Ile	Phe	Pro 110	Asp	Ser
Pro	Gly	Gly 115	Thr	Ser	Tyr	Glu	Arg 120	Tyr	Asp	Cys	Tyr	Lys 125	Val	Pro	Glu
Trp	Cys 130	Leu	Asp	Asp	Trp	His 135	Pro	Ser	Glu	Lys	Ala 140	Met	Tyr	Pro	Asp
Tyr 145	Phe	Ala	Lys	Arg	Glu 150	Gln	Trp	Lys	Lys	Leu 155	Arg	Arg	Glu	Ser	Trp 160
Glu	Arg	Glu	Val	Lys 165	Gln	Leu	Gln	Glu	Glu 170	Thr	Pro	Pro	Gly	Gly 175	Pro
Leu	Thr	Glu	Ala	Leu	Pro	Pro	Ala	Arg	Lys	Glu	Gly	Asp	Leu	Pro	Pro



			180					185					190			
Leu	Trp	Trp	Tyr	Ile	Val	Thr	Arg	Pro	Arg	Glu	Arg	Pro	Met			
		195					200					205				

<210> 285  
 <211> 139  
 <212> PRT  
 <213> Homo sapiens

<400> 285

Pro	Leu	Val	Pro	Ser	Phe	Pro	Ser	Ala	Val	Ser	Ser	Thr	Val	Leu	Ser	
1				5					10					15		
Trp	Gln	Ser	Asn	Gln	Asp	Thr	Leu	Pro	Ser	Gln	Lys	Asp	Ala	Ser	His	
			20					25					30			
Leu	Ser	Thr	Ile	Leu	Gly	Pro	Cys	Ser	Asn	Arg	Ile	Ser	His	Arg	Arg	
		35					40					45				
Cys	Pro	Gln	Glu	Ser	Gln	Gly	Arg	Cys	Met	Ala	Val	Asp	Ala	Asp	Gly	
	50					55					60					
Thr	Arg	Ile	Leu	Pro	Arg	Pro	Pro	Ser	Ala	Ala	Gly	Trp	Pro	Ser	Pro	
65					70					75					80	
Tyr	Pro	Phe	His	Ser	Tyr	Val	Leu	Gln	Thr	Gly	Leu	Ser	Ser	Asn	Lys	
				85					90					95		
Gln	Ser	Ile	Gly	Ile	Cys	Leu	Ser	Gly	Arg	Thr	Thr	Thr	Arg	Gly	Gly	
			100					105					110			
Val	Ala	Pro	Ala	Tyr	Lys	Ala	Ala	Thr	Pro	Phe	Ala	Asp	Gly	Ser	Gly	
		115					120					125				
Arg	Val	Pro	Thr	Pro	Arg	Thr	Pro	Leu	Arg	Arg						
	130					135										

<210> 286  
 <211> 80  
 <212> PRT  
 <213> Homo sapiens

<400> 286

Leu	Met	Met	Thr	Ile	Tyr	Ala	Leu	Ser	Asn	Glu	Phe	Ala	Phe	Lys	Ile	
1				5					10					15		
Asn	Glu	Glu	Gln	Leu	Ser	Phe	Phe	Pro	Leu	Leu	Ser	Val	Gln	Leu	Trp	
			20					25					30			
His	Ala	Gln	Arg	Phe	Leu	Leu	Asp	Ser	Ser	Trp	Ser	Gly	Val	Ile	Pro	
		35					40					45				
Phe	Phe	Phe	Ser	Cys	Ser	Cys	Leu	Pro	Phe	Leu	Tyr	Pro	Pro	Arg	Trp	
	50					55					60					
Arg	Gln	Ile	His	Asp	Leu	Lys	Asp	Thr	Gln	Tyr	Leu	Leu	Asn	Ser	Ser	
65					70					75					80	

<210> 287  
 <211> 80

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

Leu 1	Met	Met	Thr	Ile 5	Tyr	Ala	Leu	Ser	Asn 10	Glu	Phe	Ala	Phe	Lys 15	Ile
Asn	Glu	Glu	Gln 20	Leu	Ser	Phe	Phe	Pro 25	Leu	Leu	Ser	Val	Gln 30	Leu	Trp
His	Ala	Gln 35	Arg	Phe	Leu	Leu	Asp 40	Ser	Ser	Trp	Ser	Gly 45	Val	Ile	Pro
Phe	Phe 50	Phe	Ser	Cys	Ser	Cys 55	Leu	Pro	Phe	Leu	Tyr 60	Pro	Pro	Lys	Trp
Arg 65	Gln	Ile	His	Asp	Leu 70	Lys	Asp	Thr	Gln	Tyr 75	Leu	Leu	Asn	Ser	Ser 80

&lt;210&gt; 288

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 288

Arg 1	Leu	Ser	Cys	Ala 5	Gly	Thr	Leu	Ser	Gly 10	Ser	Gly	Pro	His	Pro 15	Ser
Arg	Arg	Leu	Thr 20	Gln	Gly	Arg	Trp	Val 25	Arg	Lys	Ser	Arg	Val 30	Ala	Met
Glu	Lys	Ile 35	Pro	Val	Ser	Ala	Phe 40	Leu	Leu	Leu	Val	Ala 45	Leu	Ser	Tyr
Thr 50	Leu	Ala	Arg	Asp	Thr	Thr 55	Val	Lys	Pro	Gly	Ala 60	Lys	Lys	Asp	Thr
Lys 65	Asp	Ser	Arg	Pro	Lys 70	Leu	Pro	Gln	Thr	Leu 75	Ser	Arg	Gly	Trp	Gly 80
Asp	Gln	Leu	Ile	Trp 85	Thr	Gln	Thr	Tyr	Glu 90	Glu	Ala	Leu	Tyr	Lys 95	Ser
Lys	Thr	Ser	Asn 100	Lys	Pro	Leu	Met	Ile 105	Ile	His	His	Leu	Asp 110	Glu	Cys
Pro	His	Ser 115	Gln	Ala	Leu	Lys	Lys 120	Val	Phe	Ala	Glu	Asn 125	Lys	Glu	Ile
Gln	Lys 130	Leu	Ala	Glu	Gln	Phe 135	Val	Leu	Leu	Asn	Leu 140	Val	Tyr	Glu	Thr
Thr 145	Asp	Lys	His	Leu	Ser 150	Pro	Asp	Gly	Gln	Tyr 155	Val	Pro	Arg	Ile	Met 160
Phe	Val	Asp	Pro	Ser 165	Leu	Thr	Val	Arg	Ala 170	Asp	Ile	Thr	Gly	Arg 175	Tyr
Ser	Asn	Arg	Leu 180	Tyr	Ala	Tyr	Glu	Pro 185	Ala	Asp	Thr	Ala	Leu 190	Leu	Leu

Asp Asn Met Lys Lys Ala Leu Lys Leu Leu Lys Thr Glu Leu  
195 200 205

<210> 289

<211> 77

<212> PRT

<213> Homo sapiens

<400> 289

Gly 1	Asn	Pro	Glu	Leu 5	Pro	Trp	Arg	Lys	Phe 10	Gln	Cys	Gln	His	Ser 15	Cys
Ser	Leu	Trp	Pro 20	Ser	Pro	Thr	Leu	Trp 25	Pro	Glu	Ile	Pro	Gln 30	Ser	Asn
Leu	Glu	Pro 35	Lys	Arg	Thr	Gln	Arg 40	Thr	Leu	Asp	Pro	Asn 45	Cys	Pro	Arg
Pro	Ser 50	Pro	Glu	Val	Gly	Val 55	Thr	Asn	Ser	Ser	Gly 60	Leu	Arg	His	Met
Lys 65	Lys	Leu	Tyr	Ile	Asn 70	Pro	Arg	Gln	Ala	Thr 75	Asn	Pro			

<210> 290

<211> 160

<212> PRT

<213> Homo sapiens

<400> 290

Gly 1	Gly	Xxx	Gly	Xxx 5	Gln	Leu	Leu	Xxx	Pro 10	Xxx	Ala	Xxx	Gln	Gly 15	Xxx
Pro	Ala	Ala	Ser 20	Cys	Xxx	Xxx	Gln	Asp 25	Val	His	Leu	Xxx	Arg 30	Cys	Xxx
Thr	Val	Val 35	Arg	Trp	Tyr	Gln	Arg 40	Ile	Thr	Gly	Met	Pro 45	Xxx	Xxx	Ala
Pro	Thr 50	Arg	Asn	Phe	Ser	Lys 55	Phe	Gln	Arg	Xxx	Val 60	Met	Asp	Leu	His
Gly 65	Phe	Pro	Lys	Glu	Xxx 70	Gly	Gln	Xxx	Glu	Xxx 75	Gln	Glu	Xxx	Leu	Gln 80
Trp	Glu	Gly	Arg	Ser 85	Ser	Ser	Gly	Lys	Cys 90	Arg	Ile	Ser	Xxx	Ser 95	Xxx
Leu	Pro	Xxx	Ser 100	Thr	Ile	Xxx	Xxx	Phe 105	Leu	Lys	Xxx	Xxx	Trp 110	Xxx	Xxx
Ile	Arg	Xxx 115	Gln	Ser	Pro	Xxx	Thr 120	Trp	Xxx	Arg	Thr	Tyr 125	Leu	Arg	Leu
Gly	Ser 130	Ile	Ser	Glu	Phe	Ser 135	Pro	Gly	Ser	Cys	Leu 140	Pro	Asn	Trp	Leu
Glu 145	Gly	Lys	Pro	Arg	Met 150	Thr	Xxx	Ala	Lys	Trp 155	Pro	Lys	Phe	Phe	Leu 160

<210> 291

<211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 291

Arg 1	His	Xxx	Pro	Leu 5	Xxx	Leu	Gly	Xxx	His 10	Gly	His	Arg	Ala	His 15	Ser
Cys	Leu	Gly	Trp 20	Ser	Gln	Xxx	Ala	Leu 25	Trp	Asp	Xxx	Ala	Trp 30	Gly	Leu
Xxx	Xxx	Xxx 35	Gly	Ser	Xxx	Gln	Xxx 40	Arg	Lys	Lys	Glu	Ala 45	Xxx	Trp	Cys
Val	Xxx 50	Val	Gly	Xxx	Val	Gly 55	Xxx	Cys	Xxx	Xxx	Pro 60	Xxx	Glu	Xxx	Met
Xxx 65	Xxx	Gly	Phe	Glu	Gln 70	Asn	Xxx	Xxx	Gly	Pro 75	Xxx	Asn	Xxx	Xxx	Val 80
Ser	Xxx	Leu	Gly	Xxx 85	Xxx	Xxx	Trp	Asn	Arg 90	Xxx	Ala	Glu	Lys	Asn 95	Met
Xxx	Gly	Cys	Cys 100	Ala	Lys	Xxx	Val	Asn 105	Xxx	Xxx	Met	Asp	His 110	Xxx	Xxx
Gly	Phe	Gln 115	Xxx	Arg	Gln	Ile	Arg 120	Gly	Leu	Cys	Ser	His 125	Ala	His	Thr
Gly	Xxx 130	Asn	Cys	His	Val	Ser 135	Xxx	Ser	Gly	Ser	Asp 140	Thr	Gln	Leu	Cys
Xxx 145	Gly	Leu	Ser	Phe	Met 150										

<210> 292  
 <211> 86  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Arg 1	Ala	Ala	Lys	Ile 5	Leu	Lys	Gly	Gly	Leu 10	Gln	Glu	Val	Ala	Glu 15	Gln
Leu	Glu	Leu	Glu 20	Arg	Ile	Gly	Pro	Gln 25	His	Gln	Ala	Gly	Ser 30	Asp	Ser
Leu	Leu	Thr 35	Gly	Met	Ala	Phe	Phe 40	Lys	Met	Arg	Glu	Met 45	Phe	Phe	Glu
Asp	His 50	Ile	Asp	Asp	Ala	Lys 55	Tyr	Cys	Gly	His	Leu 60	Tyr	Gly	Leu	Gly
Ser 65	Gly	Ser	Ser	Tyr	Val 70	Gln	Asn	Gly	Thr	Gly 75	Asn	Ala	Tyr	Glu	Glu 80
Glu	Ala	Asn	Lys	Gln 85	Ser										

<210> 293  
 <211> 64

<212> PRT  
 <213> Homo sapiens

<400> 293

Ile	Lys	Ala	Lys	Phe	Asn	Leu	Asn	Ala	Phe	Phe	Phe	Phe	Phe	Leu	Leu
1				5					10					15	
Arg	Ser	Glu	Ile	Gly	Thr	Val	Ile	Leu	Ser	Thr	Glu	Arg	Gln	Thr	Ile
			20					25					30		
Lys	Trp	Ala	Met	Lys	Gly	Gly	Gly	Lys	Val	Leu	Ser	Ile	Val	Arg	Gly
		35					40					45			
Ile	Gln	Pro	Glu	Ile	Lys	Pro	Ile	Tyr	Lys	His	Val	Cys	Ser	Ser	Lys
	50					55					60				

<210> 294  
 <211> 226  
 <212> PRT  
 <213> Homo sapiens

<400> 294

Ala	Ser	Thr	Ile	Met	Asp	Leu	Leu	Phe	Gly	Arg	Arg	Lys	Thr	Pro	Glu
1				5					10					15	
Glu	Leu	Leu	Arg	Gln	Asn	Gln	Arg	Ala	Leu	Asn	Arg	Ala	Met	Arg	Glu
			20					25					30		
Leu	Asp	Arg	Glu	Arg	Gln	Lys	Leu	Glu	Thr	Gln	Glu	Lys	Lys	Ile	Ile
		35					40					45			
Ala	Asp	Ile	Lys	Lys	Met	Ala	Lys	Gln	Gly	Gln	Met	Asp	Ala	Val	Arg
	50					55					60				
Ile	Met	Ala	Lys	Asp	Leu	Val	Arg	Thr	Arg	Arg	Tyr	Val	Arg	Lys	Phe
65					70					75					80
Val	Leu	Met	Arg	Ala	Asn	Ile	Gln	Ala	Val	Ser	Leu	Lys	Ile	Gln	Thr
				85					90					95	
Leu	Lys	Ser	Asn	Asn	Ser	Met	Ala	Gln	Ala	Met	Lys	Gly	Val	Thr	Lys
			100					105					110		
Ala	Met	Gly	Thr	Met	Asn	Arg	Gln	Leu	Lys	Leu	Pro	Gln	Ile	Gln	Lys
		115					120					125			
Ile	Met	Met	Glu	Phe	Glu	Arg	Gln	Ala	Glu	Ile	Met	Asp	Met	Lys	Glu
	130					135					140				
Glu	Met	Met	Asn	Asp	Ala	Ile	Asp	Asp	Pro	Met	Gly	Asp	Glu	Glu	Asp
145					150					155					160
Glu	Glu	Glu	Ser	Asp	Ala	Val	Val	Ser	Gln	Val	Leu	Asp	Glu	Leu	Gly
				165					170					175	
Leu	Ser	Leu	Thr	Asp	Glu	Leu	Ser	Asn	Leu	Pro	Ser	Thr	Gly	Gly	Ser
			180					185					190		
Leu	Ser	Val	Ala	Ala	Gly	Gly	Lys	Lys	Ala	Glu	Ala	Ala	Ala	Ser	Ala
		195					200					205			

Leu	Ala	Asp	Ala	Asp	Ala	Asp	Leu	Glu	Glu	Arg	Leu	Lys	Asn	Leu	Arg
	210					215					220				
Arg	Asp														
225															

<210> 295  
 <211> 166  
 <212> PRT  
 <213> Homo sapiens

<400> 295

Lys	Ile	Leu	Gly	Ile	His	Trp	Leu	Ser	Arg	Ser	Gly	Arg	Gly	Thr	Gln
1				5					10					15	
Ser	Leu	Arg	Arg	Phe	Leu	Ser	Arg	Ser	Ser	Arg	Ser	Ala	Ser	Ala	Ser
			20					25					30		
Ala	Arg	Ala	Glu	Ala	Ala	Ala	Ser	Ala	Phe	Phe	Pro	Pro	Ala	Ala	Thr
		35					40					45			
Leu	Ser	Glu	Pro	Pro	Val	Glu	Gly	Arg	Phe	Asp	Ser	Ser	Ser	Val	Arg
	50					55					60				
Leu	Ser	Pro	Ser	Ser	Ser	Arg	Thr	Trp	Asp	Thr	Thr	Ala	Ser	Leu	Ser
65					70					75					80
Ser	Ser	Ser	Ser	Ser	Ser	Pro	Met	Gly	Ser	Ser	Met	Ala	Ser	Phe	Ile
				85					90					95	
Ile	Ser	Ser	Phe	Ile	Ser	Met	Ile	Ser	Ala	Cys	Arg	Ser	Asn	Ser	Ile
			100					105					110		
Met	Ile	Phe	Trp	Ile	Trp	Gly	Asn	Phe	Ser	Cys	Leu	Phe	Met	Val	Pro
		115					120					125			
Met	Ala	Leu	Val	Thr	Pro	Phe	Met	Ala	Cys	Ala	Ile	Glu	Leu	Leu	Asp
	130					135					140				
Leu	Ser	Val	Trp	Ile	Leu	Arg	Asp	Thr	Ala	Trp	Met	Leu	Ala	Arg	Ile
145					150					155					160
Asn	Thr	Asn	Leu	Arg	Thr										
				165											

<210> 296  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 296

Lys	Pro	Glu	Gly	Ala	Arg	Arg	Val	Gln	Phe	Val	Met	Gly	Leu	Phe	Gly
1				5					10					15	
Lys	Thr	Gln	Glu	Lys	Pro	Pro	Lys	Glu	Leu	Val	Asn	Glu	Trp	Ser	Leu
			20					25					30		
Lys	Ile	Arg	Lys	Glu	Met	Arg	Val	Val	Asp	Arg	Gln	Ile	Arg	Asp	Ile
		35					40					45			
Gln	Arg	Glu	Glu	Glu	Lys	Val	Lys	Arg	Ser	Val	Lys	Asp	Ala	Ala	Lys

50					55					60						
Lys 65	Gly	Gln	Lys	Asp	Val 70	Cys	Ile	Val	Leu	Ala 75	Lys	Glu	Met	Ile	Arg 80	
Ser	Arg	Lys	Ala	Val 85	Ser	Lys	Leu	Tyr	Ala 90	Ser	Lys	Ala	His	Met 95	Asn	
Ser	Val	Leu	Met 100	Gly	Met	Lys	Asn	Gln 105	Leu	Ala	Val	Leu	Arg 110	Val	Ala	
Gly	Ser	Leu 115	Gln	Lys	Ser	Thr	Glu 120	Val	Met	Lys	Ala	Met 125	Gln	Ser	Leu	
Val	Lys 130	Ile	Pro	Glu	Ile	Gln 135	Ala	Thr	Met	Arg	Glu 140	Leu	Ser	Lys	Glu	
Met 145	Met	Lys	Ala	Gly	Ile 150	Ile	Glu	Glu	Met	Leu 155	Glu	Asp	Thr	Phe	Glu 160	
Ser	Met	Asp	Asp	Gln 165	Glu	Glu	Met	Glu	Glu 170	Glu	Ala	Glu	Met	Glu 175	Ile	
Asp	Arg	Ile	Leu 180	Phe	Glu	Ile	Thr	Ala 185	Gly	Ala	Leu	Gly	Lys 190	Ala	Pro	
Ser	Lys	Val 195	Thr	Asp	Ala	Leu	Pro 200	Glu	Pro	Glu	Pro	Pro 205	Gly	Ala	Met	
Ala	Ala 210	Ser	Glu	Asp	Glu	Gly 215	Glu	Glu	Glu	Glu	Ala 220	Leu	Glu	Ala	Met	
Gln 225	Ser	Arg	Leu	Ala	Thr 230	Leu	Arg	Ser								
<210> 297																
<211> 129																
<212> PRT																
<213> Homo sapiens																
<400> 297																
Leu 1	Met	Pro	Phe	Gln 5	Ser	Gln	Asn	Leu	Gln 10	Glu	Arg	Trp	Leu	Pro 15	Gln	
Arg	Met	Arg	Gly 20	Arg	Arg	Lys	Arg	Leu 25	Trp	Arg	Pro	Cys	Ser 30	Pro	Gly	
Trp	Pro	His 35	Ser	Ala	Ala	Arg	Gly 40	Cys	Leu	Pro	Arg	Trp 45	Val	Cys	Thr	
His	Ser 50	Ser	Gln	Glu	Leu	Pro 55	Phe	Tyr	Val	Ser	Leu 60	Ala	Leu	His	Leu	
Cys 65	Cys	Glu	Asp	Tyr	His 70	Phe	Gly	Glu	Gly	Ser 75	Val	Cys	Leu	Phe	Ser 80	
Phe	Ser	Ala	Gln	Val 85	Leu	Gly	Ser	Gln	Arg 90	Asp	Cys	Ser	Tyr	Lys 95	Ser	
Gly	Ile	Asn	Lys 100	Cys	Ile	Ile	Phe	Arg 105	Ser	Ile	Asp	Arg	Tyr 110	Ile	Leu	

Leu	Trp	Gly 115	Gly	Glu	Arg	Asn	Pro 120	Ser	Ala	His	Glu	Ala 125	Leu	Leu	Lys
Ile															
<210>	298														
<211>	351														
<212>	PRT														
<213>	Homo sapiens														
<400>	298														
Thr 1	Trp	Cys	Thr	Thr 5	Thr	Met	Leu	Ala	Ala 10	Arg	Leu	Val	Cys	Leu 15	Arg
Thr	Leu	Pro	Ser 20	Arg	Val	Phe	His	Pro 25	Ala	Phe	Thr	Lys	Ala 30	Ser	Pro
Val	Val	Lys 35	Asn	Ser	Ile	Thr	Lys 40	Asn	Gln	Trp	Leu	Leu 45	Thr	Pro	Ser
Arg	Glu 50	Tyr	Ala	Thr	Lys	Thr 55	Arg	Ile	Gly	Ile	Arg 60	Arg	Gly	Arg	Thr
Gly 65	Gln	Glu	Leu	Lys	Glu 70	Ala	Ala	Leu	Glu	Pro 75	Ser	Met	Glu	Lys	Ile 80
Phe	Lys	Ile	Asp	Gln 85	Met	Gly	Arg	Trp	Phe 90	Val	Ala	Gly	Gly	Ala 95	Ala
Val	Gly	Leu	Gly 100	Ala	Leu	Cys	Tyr	Tyr 105	Gly	Leu	Gly	Leu	Ser 110	Asn	Glu
Ile	Gly	Ala 115	Ile	Glu	Lys	Ala	Val 120	Ile	Trp	Pro	Gln	Tyr 125	Val	Lys	Asp
Arg	Ile 130	His	Ser	Thr	Tyr	Met 135	Tyr	Leu	Ala	Gly	Ser 140	Ile	Gly	Leu	Thr
Ala 145	Leu	Ser	Ala	Ile	Ala 150	Ile	Ser	Arg	Thr	Pro 155	Val	Leu	Met	Asn	Phe 160
Met	Met	Arg	Gly	Ser 165	Trp	Val	Thr	Ile	Gly 170	Val	Thr	Phe	Ala	Ala 175	Met
Val	Gly	Ala	Gly 180	Met	Leu	Val	Arg	Ser 185	Ile	Pro	Tyr	Asp	Gln 190	Ser	Pro
Gly	Pro	Lys 195	His	Leu	Ala	Trp	Leu 200	Leu	His	Ser	Gly	Val 205	Met	Gly	Ala
Val	Val 210	Ala	Pro	Leu	Thr	Ile 215	Leu	Gly	Gly	Pro	Leu 220	Leu	Ile	Arg	Ala
Ala 225	Trp	Tyr	Thr	Ala	Gly 230	Ile	Val	Gly	Gly	Leu 235	Ser	Thr	Val	Ala	Met 240
Cys	Ala	Pro	Ser	Glu 245	Lys	Phe	Leu	Asn	Met 250	Gly	Ala	Pro	Leu	Gly 255	Val
Gly	Leu	Gly	Leu 260	Val	Phe	Val	Ser	Ser 265	Leu	Gly	Ser	Met	Phe 270	Leu	Pro



Pro	Thr	Thr	Val	Ala	Gly	Ala	Thr	Leu	Tyr	Ser	Val	Ala	Met	Tyr	Gly
		275					280					285			
Gly	Leu	Val	Leu	Phe	Ser	Met	Phe	Leu	Leu	Tyr	Asp	Thr	Gln	Lys	Val
	290					295					300				
Ile	Lys	Arg	Ala	Glu	Val	Ser	Pro	Met	Tyr	Gly	Val	Gln	Lys	Tyr	Asp
305					310					315					320
Pro	Ile	Asn	Ser	Met	Leu	Ser	Ile	Tyr	Met	Asp	Thr	Leu	Asn	Ile	Phe
				325					330					335	
Met	Arg	Val	Ala	Thr	Met	Leu	Ala	Thr	Gly	Gly	Asn	Arg	Lys	Lys	
			340					345					350		

&lt;210&gt; 299

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

Arg	Val	Ala	Pro	Ala	Thr	Val	Val	Gly	Gly	Arg	Asn	Ile	Asp	Pro	Asn
1				5					10					15	
Glu	Asp	Thr	Lys	Thr	Arg	Pro	Arg	Pro	Thr	Pro	Arg	Gly	Ala	Pro	Met
			20					25					30		
Phe	Arg	Asn	Phe	Ser	Leu	Gly	Ala	His	Met	Ala	Thr	Val	Glu	Arg	Pro
		35					40					45			
Pro	Thr	Met	Pro	Ala	Val	Tyr	His	Ala	Ala	Leu	Met	Arg	Arg	Gly	Pro
	50					55					60				
Pro	Asn	Ile	Val	Arg	Gly	Ala	Thr	Thr	Ala	Pro	Ile	Thr	Pro	Glu	Cys
65					70					75					80
Ser	Asn	Gln	Ala	Arg	Cys	Phe	Gly	Pro	Gly	Leu	Trp	Ser	Tyr	Gly	Ile
				85					90					95	
Asp	Arg	Thr	Ser	Ile	Pro	Ala	Pro	Thr	Met	Ala	Ala	Lys	Val	Thr	Pro
			100					105					110		
Ile	Val	Thr	Gln	Glu	Pro	Leu	Ile	Met	Lys	Phe	Met	Arg	Thr	Gly	Val
		115					120					125			
Leu	Leu	Ile	Ala	Met	Ala	Asp	Lys	Ala	Val	Lys	Pro	Ile	Leu	Pro	Ala
	130					135					140				
Lys	Tyr	Ile													
145															

&lt;210&gt; 300

&lt;211&gt; 188

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 300

Arg	Arg	Leu	Glu	Val	Ser	Tyr	Arg	Gln	His	His	Phe	Arg	Val	Ser	Leu
1				5					10					15	
Ala	Pro	Trp	Ser	Lys	Met	Ala	Asp	Glu	Ala	Thr	Arg	Arg	Val	Val	Ser

20						25						30					
Glu	Ile	Pro	Val	Leu	Lys	Thr	Asn	Ala	Gly	Pro	Arg	Asp	Arg	Glu	Leu		
		35					40					45					
Trp	Val	Gln	Arg	Leu	Lys	Glu	Glu	Tyr	Gln	Ser	Leu	Ile	Arg	Tyr	Val		
	50					55					60						
Glu	Asn	Asn	Lys	Asn	Ala	Asp	Asn	Asp	Trp	Phe	Arg	Leu	Glu	Ser	Asn		
65					70					75					80		
Lys	Glu	Gly	Thr	Arg	Trp	Phe	Gly	Lys	Cys	Trp	Tyr	Ile	His	Asp	Leu		
				85					90					95			
Leu	Lys	Tyr	Glu	Phe	Asp	Ile	Glu	Phe	Asp	Ile	Pro	Ile	Thr	Tyr	Pro		
			100					105					110				
Thr	Thr	Ala	Pro	Glu	Ile	Ala	Val	Pro	Glu	Leu	Asp	Gly	Lys	Thr	Ala		
		115					120					125					
Lys	Met	Tyr	Arg	Gly	Gly	Lys	Ile	Cys	Leu	Thr	Asp	His	Phe	Lys	Pro		
	130					135					140						
Leu	Trp	Ala	Arg	Asn	Val	Pro	Lys	Phe	Gly	Leu	Ala	His	Leu	Met	Ala		
145					150					155					160		
Leu	Gly	Leu	Gly	Pro	Trp	Leu	Ala	Val	Glu	Ile	Pro	Asp	Leu	Ile	Gln		
				165					170					175			
Lys	Gly	Val	Ile	Gln	His	Lys	Glu	Lys	Cys	Asn	Gln						
			180					185									
<210> 301																	
<211> 172																	
<212> PRT																	
<213> Homo sapiens																	
<400> 301																	
Ser	Lys	Phe	Gly	His	Ile	Pro	Gly	Pro	Gln	Arg	Phe	Glu	Met	Ile	Arg		
1				5					10					15			
Gln	Ala	Tyr	Phe	Ala	Thr	Pro	Val	His	Leu	Cys	Cys	Leu	Ser	Ile	Gln		
			20					25					30				
Leu	Arg	Asn	Cys	Asn	Phe	Trp	Gly	Ser	Ser	Arg	Ile	Cys	Asp	Arg	Asn		
		35					40					45					
Val	Lys	Leu	Asp	Val	Lys	Leu	Ile	Phe	Gln	Glu	Val	Met	Asp	Ile	Pro		
	50					55					60						
Ala	Phe	Ser	Lys	Pro	Pro	Ser	Ser	Phe	Leu	Val	Gly	Leu	Gln	Ser	Glu		
65					70					75					80		
Pro	Ile	Val	Val	Ser	Ile	Leu	Val	Val	Leu	His	Ile	Pro	Asp	Lys	Gly		
				85					90					95			
Leu	Ile	Phe	Leu	Leu	Gln	Ser	Leu	His	Pro	Gln	Leu	Thr	Ile	Ser	Gly		
			100					105					110				
Ser	Gly	Val	Ser	Leu	Gln	His	Arg	Asp	Leu	Arg	His	Asn	Thr	Ser	Arg		
		115					120					125					

Gly	Phe	Ile	Arg	His	Leu	Gly	Pro	Gly	Arg	Lys	Arg	Asn	Ala	Glu	Val
	130					135					140				
Val	Leu	Pro	Val	Ala	Tyr	Leu	Lys	Ala	Pro	Ser	Ser	Leu	Leu	Trp	Glu
145					150					155					160
Asp	Glu	Thr	Leu	Gly	Cys	Cys	Lys	Thr	Ser	Phe	Glu				
				165					170						

&lt;210&gt; 302

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

Ala	Val	Arg	Arg	Arg	Gly	Ala	Leu	Ser	Leu	Ser	Val	Gly	Ala	Ala	Cys
1				5					10					15	
Gly	Leu	Val	Ala	Leu	Trp	Gln	Arg	Arg	Arg	Gln	Asp	Ser	Gly	Thr	Met
			20					25					30		
Ser	Gly	Phe	Ser	Thr	Glu	Glu	Arg	Ala	Ala	Pro	Phe	Ser	Leu	Glu	Tyr
		35					40					45			
Arg	Val	Phe	Leu	Lys	Asn	Glu	Lys	Gly	Gln	Tyr	Ile	Ser	Pro	Phe	His
	50					55					60				
Asp	Ile	Pro	Ile	Tyr	Ala	Asp	Lys	Asp	Val	Phe	His	Met	Val	Val	Glu
65					70					75					80
Val	Pro	Arg	Trp	Ser	Asn	Ala	Lys	Met	Glu	Ile	Ala	Thr	Lys	Asp	Pro
				85					90					95	
Leu	Asn	Pro	Ile	Lys	Gln	Asp	Val	Lys	Lys	Gly	Lys	Leu	Arg	Tyr	Val
			100					105					110		
Ala	Asn	Leu	Phe	Pro	Tyr	Lys	Gly	Tyr	Ile	Trp	Asn	Tyr	Gly	Ala	Ile
		115					120					125			
Pro	Gln	Thr	Trp	Glu	Asp	Pro	Gly	His	Asn	Asp	Lys	His	Thr	Gly	Cys
	130					135					140				
Cys	Gly	Asp	Asn	Asp	Pro	Ile	Asp	Val	Cys	Glu	Ile	Gly	Ser	Lys	Val
145					150					155					160
Cys	Ala	Arg	Gly	Glu	Ile	Ile	Gly	Val	Lys	Val	Leu	Gly	Ile	Leu	Ala
				165					170					175	
Met	Ile	Asp	Glu	Gly	Glu	Thr	Asp	Trp	Lys	Val	Ile	Ala	Ile	Asn	Val
			180					185					190		
Asp	Asp	Pro	Asp	Ala	Ala	Asn	Tyr	Asn	Asp	Ile	Asn	Asp	Val	Lys	Arg
		195					200					205			
Leu	Lys	Pro	Gly	Tyr	Leu	Glu	Ala	Thr	Val	Asp	Trp	Phe	Arg	Arg	Tyr
	210					215					220				
Lys	Val	Pro	Asp	Gly	Lys	Pro	Glu	Asn	Glu	Phe	Ala	Phe	Asn	Ala	Glu
225					230					235					240
Phe	Lys	Asp	Lys	Asp	Phe	Ala	Ile	Asp	Ile	Ile	Lys	Ser	Thr	His	Asp
				245					250					255	

His	Trp	Lys	Ala	Leu	Val	Thr	Lys	Lys	Thr	Asn	Gly	Lys	Gly	Ile	Ser
			260					265					270		
Cys	Met	Asn	Thr	Thr	Leu	Ser	Glu	Ser	Pro	Phe	Lys	Cys	Asp	Pro	Asp
		275					280					285			
Ala	Ala	Arg	Ala	Ile	Val	Asp	Ala	Leu	Pro	Pro	Pro	Cys	Glu	Ser	Ala
	290					295					300				
Cys	Thr	Val	Pro	Thr	Asp	Val	Asp	Lys	Trp	Phe	His	His	Gln	Lys	Asn
305					310					315					320

&lt;210&gt; 303

&lt;211&gt; 85

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 303

Arg	Val	Leu	Cys	Ser	Asn	Leu	His	Phe	Cys	Ile	Arg	Pro	Ala	Trp	Tyr
1				5					10					15	
Phe	Asn	Tyr	His	Val	Lys	His	Ile	Leu	Ile	Cys	Ile	Asn	Trp	Asn	Ile
			20					25					30		
Met	Lys	Trp	Arg	Tyr	Ile	Leu	Ser	Phe	Leu	Ile	Phe	Glu	Glu	Asp	Ser
		35					40					45			
Val	Leu	Gln	Gly	Glu	Gly	Arg	Gly	Ala	Leu	Leu	Gly	Ala	Glu	Ala	Ala
	50					55					60				
His	Ser	Ala	Gly	Val	Leu	Pro	Pro	Pro	Leu	Pro	Gln	Ser	His	Gln	Pro
65					70					75					80
Ala	Arg	Gly	Ala	Asp											
				85											

&lt;210&gt; 304

&lt;211&gt; 247

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 304

Gly	Ser	Ser	Gly	Ser	Arg	Phe	Glu	Val	Val	Val	Val	Leu	Glu	Glu	Arg
1				5					10					15	
Arg	Gly	Gly	Arg	Gly	Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser
			20					25					30		
Arg	Gly	Lys	Arg	Glu	Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Gly
		35					40					45			
Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	Gly
	50					55					60				
Thr	Val	Lys	Asp	Glu	Leu	Thr	Glu	Ser	Pro	Lys	Tyr	Ile	Gln	Lys	Gln
65					70					75					80
Ile	Ser	Tyr	Asn	Tyr	Ser	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	Glu	Glu
				85					90					95	

Thr	Pro	Glu	Gly	Glu	Glu	His	His	Pro	Val	Ala	Asp	Thr	Glu	Asn	Lys
			100					105					110		
Glu	Asn	Glu	Val	Glu	Glu	Val	Lys	Glu	Glu	Gly	Pro	Lys	Glu	Met	Thr
		115					120					125			
Leu	Asp	Glu	Trp	Lys	Ala	Ile	Gln	Asn	Lys	Asp	Arg	Ala	Lys	Val	Glu
	130					135					140				
Phe	Asn	Ile	Arg	Lys	Pro	Asn	Glu	Gly	Ala	Asp	Gly	Gln	Trp	Lys	Lys
145					150					155					160
Gly	Phe	Val	Leu	His	Lys	Ser	Lys	Ser	Glu	Glu	Ala	His	Ala	Glu	Asp
				165					170					175	
Ser	Val	Met	Asp	His	His	Phe	Arg	Lys	Pro	Ala	Asn	Asp	Ile	Thr	Ser
			180					185					190		
Gln	Leu	Glu	Ile	Asn	Phe	Gly	Asp	Leu	Gly	Arg	Pro	Gly	Arg	Gly	Gly
		195					200					205			
Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Pro	Asn	Arg	Gly
	210					215					220				
Ser	Arg	Thr	Asp	Lys	Ser	Ser	Ala	Ser	Ala	Pro	Asp	Val	Asp	Asp	Pro
225					230					235					240
Glu	Ala	Phe	Pro	Ala	Leu	Ala									
				245											

&lt;210&gt; 305

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 305

Ser	Phe	Gly	Ile	Leu	Lys	His	Ala	Lys	Ala	Leu	Asn	Arg	Arg	Val	His
1				5					10					15	
Lys	Gly	Thr	Arg	Val	Val	Leu	Trp	His	Pro	Val	Lys	Pro	Glu	Leu	Gly
			20					25					30		
Met	Pro	Leu	Gly	His	Pro	His	Gln	Glu	Gln	Lys	His	Leu	Thr	Cys	Arg
		35					40					45			
Ser	Cys	Cys	His	Gly	Leu	Gly	Ala	His	His	Ala	His	Val	His	Leu	Val
	50					55					60				
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&lt;210&gt; 306

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 306

Ala	Thr	Arg	Gly	Ala	Glu	Gln	Asp	Gly	Gly	Ala	Ser	Ala	Ala	Arg	Pro
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Arg	Arg	Arg	Trp	Ala	Gly	Gly	Leu	Leu	Gln	Arg	Ala	Ala	Pro	Cys	Ser

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Leu	Leu	Pro 35	Arg	Leu	Arg	Thr	Trp 40	Thr	Ser	Ser	Ser	Asn 45	Arg	Ser	Arg
Glu	Asp 50	Ser	Trp	Leu	Lys	Ser 55	Leu	Phe	Val	Arg	Lys 60	Val	Asp	Pro	Arg
Lys 65	Asp	Ala	His	Ser	Asn 70	Leu	Leu	Ala	Lys	Lys 75	Glu	Thr	Ser	Asn	Leu 80
Tyr	Lys	Leu	Gln	Phe 85	His	Asn	Val	Lys	Pro 90	Glu	Cys	Leu	Glu	Ala 95	Tyr
Asn	Lys	Ile	Cys 100	Gln	Glu	Val	Leu	Pro 105	Lys	Ile	His	Glu	Asp 110	Lys	His
Tyr	Pro	Cys 115	Thr	Leu	Val	Gly	Thr 120	Trp	Asn	Thr	Trp	Tyr 125	Gly	Glu	Gln
Asp	Gln 130	Ala	Val	His	Leu	Trp 135	Arg	Tyr	Glu	Gly	Gly 140	Tyr	Pro	Ala	Leu
Thr 145	Glu	Val	Met	Asn	Lys 150	Leu	Arg	Glu	Asn	Lys 155	Glu	Phe	Leu	Glu	Phe 160
Arg	Lys	Ala	Arg	Ser 165	Asp	Met	Leu	Leu	Ser 170	Arg	Lys	Asn	Gln	Leu 175	Leu
Leu	Glu	Phe	Ser 180	Phe	Trp	Asn	Glu	Pro 185	Val	Pro	Arg	Ser	Gly 190	Pro	Asn
Ile	Tyr	Glu 195	Leu	Arg	Ser	Tyr	Gln 200	Leu	Arg	Pro	Gly	Thr 205	Met	Ile	Glu
Trp	Gly 210	Asn	Tyr	Trp	Ala	Arg 215	Ala	Ile	Arg	Phe	Arg 220	Gln	Asp	Gly	Asn
Glu 225	Ala	Val	Gly	Gly	Phe 230	Phe	Ser	Gln	Ile	Gly 235	Gln	Leu	Tyr	Met	Val 240
His	His	Leu	Trp	Ala 245	Tyr	Arg	Asp	Leu	Gln 250	Thr	Arg	Glu	Asp	Ile 255	Arg
Asn	Ala	Ala	Trp 260	His	Lys	His	Gly	Trp 265	Glu	Glu	Leu	Val	Tyr 270	Tyr	Thr
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Asp	His	Asp	Ser 20	Gly	Phe	His	Phe	Leu 25	Asn	Lys	Trp	Asn	Cys 30	Val	Ile
Tyr	Gln	Phe 35	Leu	Pro	Ala	Met	Phe 40	Val	Pro	Cys	Cys	Ile 45	Pro	Tyr	Val
Phe	Pro 50	Gly	Leu	Lys	Ile	Pro 55	Val	Ser	Pro	Lys	Met 60	Val	His	His	Val
Gln 65	Leu	Pro	Asn	Leu	Arg 70	Glu	Glu	Ser	Ser	Asp 75	Gly	Phe	Val	Thr	Ile 80
Leu	Ser	Glu	Ala	Asp 85	Cys	Thr	Ser	Pro	Val 90	Ile	Ala	Pro	Phe	Asn 95	His
Gly	Ser	Trp	Ser 100	Glu	Leu	Val	Arg	Pro 105	Glu	Phe	Ile	Tyr	Ile 110	Arg	Ser
Gly	Ser	Trp 115	His	Arg	Leu	Ile	Pro 120	Glu	Thr	Glu	Leu	Gln 125	Gln	Glu	Leu
Ile	Leu 130	Pro	Gly	Glu	Lys	His 135	Val	Thr	Ser	Cys	Leu 140	Thr	Lys	Phe	Gln
Lys 145	Phe	Leu	Ile	Phe	Ser 150	Glu	Phe	Ile	His	Asp 155	Phe	Cys	Glu	Gly	Trp 160
Ile	Ala	Ser	Phe	Ile 165	Pro	Pro	Glu	Val	Asp 170	Ser	Leu	Val	Leu	Leu 175	Ala
Ile	Pro	Arg	Val 180	Pro	Ser	Pro	His	Gln 185	Ser	Thr	Arg	Val	Val 190	Phe	Ile
Phe	Val	Asn 195	Leu	Trp	Gln	His	Leu 200	Leu	Thr	Asn	Phe	Val 205	Val	Cys	Phe